

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:01:02 ; Search time 17 seconds
(without alignments)
3568.337 Million cell updates/sec

Title: US-10-026-188-8
Perfect score: 6093
Sequence: 1 MDVQPRPGSPGDAEDRRE.....HRGGLDGEQPGAGPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2039	33.5	1503	1	TRL2_HUMAN
2	1074	17.6	2032	1	TRFG_CABEL
3	662	10.9	1017	1	TRL3_HUMAN
4	325	5.3	1275	1	TRP_DROME
5	294	4.8	1418	1	CE1L_CAEEL
6	266.5	4.4	1124	1	TRL2_DROME
7	264.5	4.3	1172	1	TRL2_MOUSE
8	247	4.1	974	1	TRP5_HUMAN
9	247	4.1	975	1	TRP5_MOUSE
10	247	4.1	975	1	TRP2_MOUSE
11	240	3.9	1027	1	TRL1_CAEEL
12	226	3.7	981	1	TRL4_BOVIN
13	223.5	3.7	977	1	TRL4_HUMAN
14	220	3.6	974	1	TRL4_MOUSE
15	220	3.6	977	1	TRL4_RAT
16	220	3.6	977	1	TRL4_MOUSE
17	204.5	3.4	836	1	TRP3_MOUSE
18	201	3.3	931	1	TRP6_HUMAN
19	200	3.3	862	1	TRP7_HUMAN
20	194	3.2	862	1	TRP7_MOUSE
21	193.5	3.2	736	1	TRP3_RAT
22	192.5	3.2	848	1	TRP3_HUMAN
23	190	3.1	930	1	TRP6_MOUSE
24	184.5	3.0	759	1	TRP1_RABIT
25	177	2.9	793	1	TRP1_BOVIN
26	176.5	2.9	759	1	TRP1_RAT
27	176.5	2.9	793	1	TRP1_HUMAN
28	176.5	2.9	809	1	TRP1_MOUSE
29	164.5	2.7	3678	1	DMD_MOUSE
30	159	2.6	432	1	TRP2_BOVIN
31	155	2.5	968	1	PKD2_HUMAN
32	152.5	2.5	966	1	PKD2_MOUSE
33	149	2.4	3680	1	DMD_CANFA

RESULT 1

ID	TRL2_HUMAN	STANDARD;	PRT;	1503 AA.
AC	O94759; O96KNE;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Long transient receptor potential channel 2 (Ltrpc2) (Transient receptor potential channel 7) (TrpC7).			
GN	TRPM2 OR LTRPC2 OR TRPC7 OR KNP3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Brain;			
RX	MEDLINE=99026133; PubMed=9806937;			
RA	Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F., Shimizu N.;			
RA	"Molecular cloning of a novel putative Ca2+ channel protein (TRPC7) highly expressed in brain.";			
RL	Genomics 54:124-131(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=22075135; PubMed=11960981;			
RA	Whehage E., Eisefeld J., Heiner I., Jungling E., Zitt C., Luckhoff A.;			
RT	"Activation of the cation channel long transient receptor potential channel 2 (LTPC2) by hydrogen peroxide: A splice variant reveals a mode of activation independent of ADP-ribose.";			
RL	J. Biol. Chem. 277:23150-23156(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20289799; PubMed=10830953;			
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P., Scharfe J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Vaspo M.-L.;			
RT	"The DNA sequence of human chromosome 21.";			
RL	Nature 405:311-319(2000).			
CC	!- FUNCTION: May be a calcium channel.			
CC	!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Comment=Additional isoforms seem to exist;			
CC	Name=1;			
CC	isoId=O94759-1; Sequence=Displayed;			
CC	Name=2;			

34	138	2.3	830	1	VPP3_HUMAN	Q13488 h vacuolar
35	134	2.2	5596	1	MDN1_HUMAN	Q9nu22 homo sapien
36	130.5	2.1	2390	1	SPCP_HUMAN	Q15020 homo sapien
37	129.5	2.1	1261	1	APAF_BRARE	Q919h8 brachydanio
38	129.5	2.1	3685	1	DMD_HUMAN	P11532 homo sapien
39	126.5	2.1	2388	1	SPCP_RAT	Q9qwn8 rattus norv
40	126	2.1	5065	1	EPPL_HUMAN	P58107 homo sapien
41	124.5	2.0	1835	1	CCAI_RAT	Q920y8 rattus norv
42	123.5	2.0	2223	1	CCAI_HUMAN	Q9p0x4 homo sapien
43	123	2.0	1060	1	AZ11_MOUSE	Q62036 mus musculu
44	123	2.0	2019	1	CIN5_RAT	P15389 rattus norv
45	121	2.0	805	1	P2Li_HUMAN	Q9p019 homo sapien

ALIGNMENTS

Db 1244 RSRNNRSDMSKTSVIFGSDPNLSKLQKGNITSTDRPNMBQPGQTRKIKORRRFYEFY 1303

Qy 729 GAPVTVLGNVVMFAFLFTYVLLYDRPPPGQSGPEVTLVFWVFTLLVLEIRQGF 788

Db 1304 SAPISTFWSWTISFILITFTYVLLV--KTTPR-PTVIEVILYVAAFGLEQVKLIIM 1360

Qy 789 TDETHLVKKFTLVGNWNNKDMVAIFLFIYVGTCTRLMPSAFBAGRTVLAMDFMFTLR 848

Db 1361 SDAXP-FYEKIRTVCGFWNCVTILAIIFYIVGFFMRCFGSV-AYGRVILACDSVLWTMK 1418

Qy 849 LIHFAHKLQKGLPIIVERMKDVFFLFLSVLWVAYGTTQALLPHDGRLEWIF-R 907

Db 1419 LLDYMSVHPKLGIVTVMAGKIQMNSYIIVLVTLISFGIAROSITYP-DETHWILVR 1477

Qy 908 RVLRYRPLQIFGQIPLEIDARVNCSTH-----PULLEDSP---SCPSLYANWL 954

Db 1478 NIFKPTFMYLGEVYADEID---TCGDEAWDQHLNGPVLNGITGLSCVGY--WI 1531

Qy 955 VILLVTVLLVTVNLLNLLIAMSFTYQVVGNNADMFQRYNLIIVEYHERPALAPPF 1014

Db 1532 PPLMTFTLLANILLMSLJAIENHIFDATDMSQIWLQRYQVQVMEYESTPFLPPL 1591

Qy 1015 ILLSHLSITLR---RVFKKAEHREHLERDLPDLD----QKVVTVETVQKENFL-SK 1065

Db 1592 TPLVHGVLLIQLFVTRTSCSKSQBNPMFDFSLKFLDNDQIEKLHDFEEDCMEDLARQK 1651

Qy 1066 MEKRRRSEGBVLKRTAHR-----VDFAIKYLG---LREQEKRIKCLBSQINYSVL 1115

Db 1652 LNEKNTSNEQIRLADIRTDQILNRLIDLQAKSMGRDVINDVESRLASVEKAQN---EI 1708

Qy 1116 VSSVADVLAAQGGPRSSQHC 1135

Db 1709 LECVRALLNQNNAPTAIGRC 1728

RESULT 3

TRL3 HUMAN

ID - TRP DROME STANDARD; PRT; 1017 AA.

AC Q9HCF6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Long transient receptor potential channel 3 (LTrpC3) (Fragment).

GN TRPM3 OR LTRPC3 OR KIAA1616.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=20450683; PubMed=10997877;

RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes.

RT XVII. The complete sequences of 100 new cDNA clones from brain which

RT code for large proteins in vitro.";

RL DNA Res. 7:273-281(2000).

CC -!- FUNCTION: May be a calcium channel.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -!- SIMILARITY: Belongs to the transient receptor family. LTrpC

CC subfamily.

CC -----

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CC -----

DR EMBL; AB046836; BAB13442.1; -

DR Genew; HGNC:17992; TRPM3.

DR InterPro; IPR002111; Cat_channel_Trlp.

DR InterPro; IPR005821; Ion_trans.

DR Pfam; PF00520; ion trans; 1.

KW Ionic channel; Transmembrane; Ion transport; Calcium channel.

FT NON TER 1

FT TRANSMEM 80 100 POTENTIAL.

FT TRANSMEM 183 203 POTENTIAL.

FT TRANSMEM 250 270 POTENTIAL.

FT TRANSMEM 314 334 POTENTIAL.

FT TRANSMEM 402 422 POTENTIAL.

FT TRANSMEM 453 473 POTENTIAL.

SQ SEQUENCE 1017 AA; 116681 MW; B088354F100A972C CRC64;

Query Match 10.9%; Score 662; DB 1; Length 1017;

Best Local Similarity 28.0%; Pred. No. 1.5e-36;

Matches 171; Conservative 135; Mismatches 247; Indels 58; Gaps 14;

Qy 576 YERLALDLPECYVNSARAFALLVRRNRCSKTTCLHLATEADAKAFFAHGQVQLTR 635

Db 10 FGQAVELLDOOSYKQDQLAKWLLTYELKNWSNATCQLQVAAKHDFIAHCSQMLLTD 69

Qy 636 IWWG--DMAAGTPTILRLIGAFPCALV---YTNLITFSEAPLRTGLE--LQDLSDSLDT 688

Db 70 MMGRRLMRKNSGLKVILGILLPSILSLFKN---KDDMPYMSQAEIHLQKEAREP 125

Qy 689 EKSPYGLQSRVELVAPRAQDRG-----PRAVLLTRWRKFWGAPVTVFLG 737

Db 126 EKPTKEKEEEDMELTAMLGRNNGESSRKDEEVSQSKHRLIPLGRKIYEFYNAPIVKFWF 185

Qy 738 NVVMYFAFLFTVTVLLVADFRPPPGQSGPEVTLVFWVFTLLVLEIRQGFDTDLTVLK 797

Db 186 YTLAYIGYLMFNIVILVKME---RWPTQRMWISYIFTLGIEKRE--ILMSBPGKLLQ 241

Qy 798 KFTLYVGDNNWKNCDMVAIFLFIYVGTCTRLMPSAFEA--GRVVLAMDPMVFTLRLIHF 856

Db 242 KVKVWLOEYWNVTDLIALLLFSVGMILRLQDQPPRSDGRVIYCVNIIYVIRLLDIEGVN 301

Qy 857 KQLGPKLIIVERMMKQVFFLFLSVLWVAYGTTQALLPHDGRLEWIFRVLRYPLQ 916

Db 302 KYLGFYVMYMGKMMIDMYFIINLVLMVSGVARQAILFENEPSWKLAKNIFMYPYMW 361

Qy 917 IFGOIPLDEIDARVNCSTHPLLEDSS-----PSCPILYANWLVLITVTELLVTVNLLM 971

Db 362 IYGSVFADQIDPPGQNETR---EDGKIQLPCKT--GAWIVPAIMACVLLVANILLV 415

Qy 972 NLLIAMSFTYQVVGNNADMFQRYNLIIVEYHERPALAPPFILLSHLSITLRVFKKE 1031

Db 416 NLLIAVNNITFEVKSISNQWKFQRYQLIMTPHERPVLPPPLIFSHMTMFIQHLCCRW 475

Qy 1032 AEHREHLERD-----LPDPLDQKVTWTVQKENFLSKMEKRRRSEGEVLRKTAIRV 1085

Db 476 RKHSDPDERDYGLKLFITDDELKKVHDFEBQCEIEYFREKDDRFNSNDRIRVTSERV 535

Qy 1086 DFIAYLGLGREQEKRIK---LESQINYSVLVSSVADVLAQGG-----PRS 1131

Db 536 ENMSRLVEEVNREHSMKASLQTVDIRLAQLEDLIGRWATALERLTGLERAESNKIRST 595

Qy 1132 SQHCGEGSQLV 1142

Db 596 SSDCTDAAYIV 606

RESULT 4

TRP DROME

ID - TRP DROME STANDARD; PRT; 1275 AA.

AC P19334;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transient receptor potential protein.

GN TRP.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_taxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=90180449; PubMed=2516726;
 RA Montell C., Rubin G.M.;
 RT "Molecular characterization of the Drosophila trp locus: a putative
 integral membrane protein required for phototransduction.";
 RL Neuron 2:1313-1323(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90148782; PubMed=2482778;
 RX Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Seaton D.,
 RA Shao D.;
 RT "Proper function of the Drosophila trp gene product during pupal
 development is important for normal visual transduction in the
 adult.";
 RL Neuron 3:81-94(1989).
 RN [3]
 RP SEQUENCE OF 1126-1275 FROM N.A.
 RX MEDLINE=88042982; PubMed=3118483;
 RA Wong F., Yuh Z.T., Schaefer E.L., Roop B.C., Ally A.H.;
 RT "Overlapping transcription units in the transient receptor potential
 locus of Drosophila melanogaster.";
 RL Somat. Cell Mol. Genet. 13:661-669(1987).
 CC -!- FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE
 CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT
 CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 MEMBRANES OF THE PHOTORECEPTOR CELLS.
 CC -!- SIMILARITY: Belongs to the transient receptor family. STpC
 subfamily.
 CC -!- SIMILARITY: Contains 2 ANK repeats.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M34394; AAA28976.1; -;
 DR EMBL; M21306; AAA56928.1; -;
 DR EMBL; M18634; AAA28977.1; -;
 DR FlyBase; FBgn0003861; trp.
 DR GO; GO:0016028; C:rhodome; IDA.
 DR GO; GO:0015279; F:store-operated calcium channel activity; NAS.
 DR GO; GO:0008377; P:light-induced release of calcium, from inte. .; IDA.
 DR GO; GO:0009416; P:response to light; IMP.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR002153; Trans receptor.
 DR InterPro; IPR004729; Trp CaChannel.
 DR Pfam; PF00023; ank; 2.
 DR Pfam; PF00520; ion trans; 1.
 DR PRINTS; PR01097; TRNSRECEPTR.
 DR SMART; SM00248; ANK; 2.
 DR TIGRFAMS; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 Vision; ANK repeat; Repeat.
 FT DOMAIN 1 366
 FT TRANSMEM 367 387
 FT POTENTIAL.
 FT DOMAIN 388 390
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 391 411
 FT POTENTIAL.
 FT DOMAIN 412 418
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 419 439
 FT POTENTIAL.
 FT DOMAIN 440 450
 FT EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	451	471	POTENTIAL.
FT	DOMAIN	472	507	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	508	528	POTENTIAL.
FT	DOMAIN	529	541	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	542	562	POTENTIAL.
FT	DOMAIN	563	638	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	639	659	POTENTIAL.
FT	DOMAIN	660	1275	EXTRACELLULAR (POTENTIAL).
FT	REPEAT	69	98	ANK 1.
FT	REPEAT	143	172	ANK 2.
FT	CONFLICT	285	288	GQRQ -> ASSE (IN REF. 2).
FT	CONFLICT	326	329	RRKQ -> PQE (IN REF. 2).
FT	CONFLICT	365	374	KPFVKFTHS -> NPLSSSRTP (IN REF. 2).
FT	CONFLICT	785	785	S -> N (IN REF. 2).
SQ	SEQUENCE	1275 AA;	142589 MW;	91CFCD9896989B1 CRC64;

Query Match 5.3%; Score 325; DB 1; Length 1275;
 Best Local Similarity 20.0%; Pred. No. 1.1e-13;
 Matches 184; Conservative 133; Mismatches 275; Indels 328; Gaps 39;

QY	274	VPKVAEK-QFKEKPSKHSFMSDIVRWTKLQNTSH-----OHLTVYDPEQGS	323
DB	48	VKKILEYQGTDKP---NINCTDPNRSALISAENENFDLMVILLENIEVGDALLHAI	104
QY	324	BEIDTVILKALVKACKSHSQPDYLDLKLAVMDRVDIKAKSEIPNGDVEWVKSCDLEEV	383
DB	105	SEEVYEAVEELLQWEETNHKEGPY-----SWEAVDRSKS-TFTVDI-----TP	147
QY	384	MYDALVSNKPEFVRLFDVNGA-----DVADFLTYGELQ-ELYSVSR	424
DB	148	LILAAHRNRYEILKILLDRGATLPMHVDKCGDECVTSTQTTDSLRHSQSRINAYRASA	207
QY	425	KSLFLDLLQKQEBEARLTLAGLTQCAREPPAGPAFSLHVSRLK--DFLQACRGFY	482
DB	208	SSLI-----ALSSRD-----PVLTVFQLSWELKRLQAMESFEARY	243
QY	483	QDGRFDRRAEKGPAKPTQOKWLLDLNQNSENPMRDLFLWAVLONRHEMATYFWAMQ	542
DB	244	TEMR---QWQDFGTS-----LLDHARTS-----MELEVMLNFNHPSHDIWCLQ	286
QY	543	EGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLVR	602
DB	287	-----RQTLER-----	292
QY	603	NRCWSKTTCLHLATEADAKAPFAHGVQAFTRIWMGDMAAGTPIRLLLGAFCLPALVYT	662
DB	293	-----LKLAIRYKOKTFVAHNVVQOLLAIIWD---GLPGFR-----	326
QY	663	NLITFSEBAPLRTGLDLDLSTDEKSPLYGLQSRVEELVEAPRAQDGRPAVFLLT	722
DB	327	-----RKQASQQLMDVVKLGCSFPPIYSL-----KVILAPDSEG-----	359
QY	723	RWRKFWGAPVTVFLGNVVMYFAFLF-----FTYVL--LYDFFRPPQG	763
DB	360	--AKEMRKPFPVKFITHSCSYMPFLMLLGAASLRVVQITFELLAFPMWLTMLDWRKHG	417
QY	764	--PSGPEVTLYFWVFTLVLEIR-----OGFTDEDTHLVKFTLVYGNWNKCDMVAIFL	817
DB	418	SUGPIELAIITYIMALIFEELKSLYSDGLE-----YIMDLNIVDIYSNMF	465
QY	818	FIVGVTCR-----MLPS--AFEAGRTVLMDFMVF	845
DB	466	VVTWILCRATAWIVHRDLWFRGIDPYFPFHWHHPDPMLLSEGAFAG-----WVF	517
QY	846	T-LRLIHIFAIKQGPKIIVVERMKDVFVFLFSLVWLVAYGVTTQALL-----	895
DB	518	SYLKLVIHIFSINPHLGLQVSLGRMIIDIKFFITYTLVFAFGCGLNQLLYAELEKN	577
QY	896	---HCHDGRLEW-----IFRRV--LYRP-----YLQIFGOIPLDEIDEARVNCSTHPL	938
DB	578	KCYHLHPDVADFDQOEKACTIWRFSNLFETSQSFLWASFLVDLVSFDLGKGS-----	632
QY	939	LLEDSPSPCPSLYANWLVILLVTLFLLVNLVNLNLIAMFSYTFQVQGNADMFWKFOR	998

```

Db 633 -----FTRFWALLMEFGSYVINIIIVLLNMLIAMSNSYQIIISERADTWEKFAFS 681
Qy 999 NLIVVEYHE-RPALAPETILLSHLSJTLRRVFKAEHKEHLERDL--PDLDQKVVTWE 1055
Db 682 QLMWSYFEDGGTIPPPFNLCNKKLRLTKLRKSPRTSKSPMRKSMERAOQLHDQVM--- 738
Qy 1056 TVQKENFLSKMEKRRDSEG 1075
Db 739 KLLVRYIT-AEQRRDDYG 757

RESULT 5
CE11 CAEEL STANDARD; PRT; 1418 AA.
AC P34641;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ced-11 protein.
GN CED-11 OR ZK512.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnhammer E., Staden K.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans.";
RL Nature 368:32-38 (1994).
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CC EMBL; Z22177; CAA80145.1; -.
DR PIR; S40764; S40764.
DR WormPep; ZK512.3; CE00409.
DR InterPro; IPR000111; Cat channel TrpL.
SQ SEQUENCE 1418 AA; 159237 MW; 4FC83B9E7ADF7788 CRC64;

Query Match
Best Local Similarity 4.8%; Score 294; DB 1; Length 1418;
Matches 222; Conservative 174; Mismatches 437; Indels 264; Gaps 45;

Qy 65 PNLVSVLGEQPPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLRHVGQVRDHS 124
Db 67 PDLIISLISHGNSLSTK--YMSVENVGLKSLFGCTWLISG-----EVNDPM 113
Qy 125 LASTSTKRVVAVGMASIGRVLHRRILLEEAEQEDFVHPYEDGGSQGLCLSLDNLSHFI 184
Db 114 SRVAGALKNVLPQLEHQAEVLH--ILVNSDD----MIASDTTNSKS---VVDTSINTLL 164
Qy 185 LV---EPGPPGKGDGLTELRLRLEKHI-----SE--ORAGYGGTCSI----- 221
Db 165 LICRKEFNDSEYETVASSIAKLRAATAVLAHPPALLIGVSEPMSPSTYGSNAAILLSP 224

```

RESULT 6

TRPL DROME

ID TRPL DROME STANDARD; PRT; 1124 AA.

AC P48994; Q9V5B2;

DT 01-FEB-1996 (Rel. 33, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Transient-receptor-potential-like protein.
 GN TRPL OR CG18345/CG1694.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 EX MEDLINE=92232293; PubMed=1314616;
 RA Phillips A.M., Bull A.L., Kelly L.E.;
 RT "Identification of a Drosophila gene encoding a calmodulin-binding
 RL protein with homology to the trp phototransduction gene.";
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler J., Caudle E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de la Chapelle B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.-H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McInerney M.P., McPherson D.,
 RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Palazzolo M., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.
 CC -!- SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
 CC -!- SIMILARITY: Belongs to the transient receptor family. STRPC
 CC subfamily.
 CC -!- SIMILARITY: Contains 2 ANK repeats.

CC EMBL; M8185; AAA28979.1; -
 DR EMBL; AE003832; BAM68793.1; -
 DR F01; JH0588; JH0588.
 DR FlyBase; Fgn0005614; trpl.
 DR GO; GO:0016021; C: integral to membrane; NAS.
 DR GO; GO:0016028; C: rhododerm; IDA.
 DR GO; GO:0015075; F: ion transporter activity; NAS.
 DR GO; GO:0015279; F: store-operated calcium channel activity; NAS.
 DR GO; GO:0006811; F: ion transport; NAS.
 DR GO; GO:0009628; F: response to abiotic stimulus; IMP.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR002153; Trans_receptor.
 DR InterPro; IPR004729; Trp_CaChannel.
 DR Pfam; PF00023; ank; 2.
 DR Pfam; PF00520; ion_trans; 1.
 DR PRINTS; PR01097; TRNSRECEPTR.
 DR SMART; SM00248; ANK; 2.
 DR TIGRfam; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW Calmodulin-binding; Vision; ANK repeat; Repeat.
 FT DOMAIN 1 340 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 341 361 POTENTIAL.
 FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 374 394 POTENTIAL.
 FT DOMAIN 395 431 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 432 452 POTENTIAL.
 FT DOMAIN 453 512 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 513 533 POTENTIAL.
 FT DOMAIN 534 548 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 549 569 POTENTIAL.
 FT DOMAIN 570 645 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 646 666 POTENTIAL.
 FT DOMAIN 667 1124 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 78 107 ANK 1.
 FT REPEAT 152 181 ANK 2.
 FT DOMAIN 710 727 CALMODULIN-BINDING (POTENTIAL).
 FT DOMAIN 809 825 CALMODULIN-BINDING (POTENTIAL).
 FT CONFLICT 228 229 II -> SS (IN REF. 1).
 SQ SEQUENCE 1124 AA; 127749 MW; AF6323BA27626583 CRC64;
 Query Match 4.4%; Score 266.5; DB 1; Length 1124;
 Best Local Similarity 19.2%; Pred. No. 7.9e-10;
 Matches 182; Conservative 146; Mismatches 269; Indels 349; Gaps 43;
 QY 295 DIVRWTKLQNTSHOHL-----LTVYDFEFGSEELDTVL-----KALVK 336
 DB 53 DMNVRRILQKALRHQHINCMDFLGRRLTL-AIDNENLEMVELLVGMVETKDALH 111
 QY 337 ACKSHSQPQDYLDLKLAV-----AWDRVDIAKSEIFNGDVEKSCDLEEVMDALV 389
 DB 112 AINAEFVEAVELLEHEELIYKEGEPYSQKVDI-NTAFAPDI-----TPMLLAH 162
 QY 390 SNKEPFEVRLFVDNGA--DVADFLTYGRLOEYRSVRSKSLFLDLQKOEAEARLTAGIG 447
 DB 163 KNFPEILLIDRGAAVVPVHDIRCG-CEECVRLTAEDSL-----RHSLSRVN 209
 QY 448 TQAREPP-----AGPPAFSLHEVSRVLKD--FLQDACRGFYQDGRGDRRAKGP 499
 DB 210 IYRALCPSLCLISNDPIITAFQLSWELRNALTEQCEKSEYMD-----LRQCQFAVD 265
 QY 500 RPTGOKMLLDNQSSENFWRDLFLWAVLQNHENWATYFWAMQEGVAAALACKILKEMS 559
 DB 266 -----LLDQTRISNE-----LAILNYDPQMSY-----EPG----- 292
 QY 560 HLETEAARATREAKYVERLALDLFSECYSNEARAFALLVRNRCWSKTTCLHLATRAD 619
 DB 293 -----DRMSL-----TRLQAISYK 307

QY 620 AKAFPAHDGVAFLTRIWDGMAAGTPIIR---LLGAFGLCPALVYTNLTIFSEAPLRTG 676
DB 308 QKKEVAHNTQOLLSSWYD---GLGFRKRSIVDKVICIAQV---AVLF----- 351
QY 677 LEDQLDLSLDTESPLYGL-----QSRVEELVEAPRAQGDGRPRAVFLLTRWRKFWGA 730
DB 352 -----PLYCLTYMCAPNCKRTQQLM-----RK----- 372
QY 731 PVTYFLGNVVMYFAFLFTVLVAV-----DERPPPGPSG 766
DB 373 PFMKFLIHASSYLFLLFI---LILVSORADDVFRIFGTTMKKELAEQLRQSGTPSK 429
QY 767 PEVTLYFWFVFLVLEERIQGFDTEDTHLVKFTLYVGDNMKCDMAIFLIVGVTCRM 826
DB 430 LELIVVMVIGFVVEEQEIPAVGMS-----YLENMWNFTDFLNSLY-VSVWC-L 479
QY 827 LPSAFEAAGRTVLAMD-----FWVFT-LRLIHIHAIHKQL 859
DB 480 RAFAYIQOATEIARDPQMAVIPREKWHDFDPQLIAEGLFAAANVFSAKLWHLFSINPHL 539
QY 860 GPKLIIVVERMKDV---FFELPFLSVMLVAYGVV-----TOALLHPHDCGRLEW-- 904
DB 540 GPLQISLGRMWIDIVKFFIYILVIFAFACGLNQLLMYFAALEKSKCVLP-GGEADWGS 598
QY 905 -----IFRRV-LYRP-----YLOIFGQIPLDEIDEARVNGSTHPLLEDSPSCPSLYAN 952
DB 599 HGDSCKMKRRFGNLFESSQSFLWASFGVGLDDFELSGIKS-----YTR 642
QY 953 WLVTLLVTLVTLNVLNMLLIAMFSYTFQVQGNADMFKFORYNLIVYHERPA-LA 1011
DB 643 FWGLIFGSGSVINIVILLNLLIAMNSYAMIDEHSDTEWKFARTKLWMSYFEDSATLP 702
QY 1012 PFTILLSLTLARVFKKAHREHLERLDPDLPQVKVTVTWVQENFLSKWKERR 1071
DB 703 PPFNVLSVKWVI-RIFKRS-----KTIQRQSKRKEBQF 739
QY 1072 DSEGEVLKTAHRVDFIAKYLGLLREQ-----EKRIKLCESQIN 1110
DB 740 SEYDNIMR-----SLVWRYVAAMHRKFENNVPVSEDDINEVKSEIN 779
RESULT 7
TRP2 MOUSE
ID TRP2 MOUSE STANDARD; PRT; 1172 AA.
AC Q9R244; Q9ES59; Q9ES60; Q9R243;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Short transient receptor potential channel 2 (Trp2) (mTrp2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=99162557; PubMed=10051594;
RA Vannier B., Peyton M., Boulay G., Brown D., Qin N., Jiang M., Zhu X.,
RA Birnbaumer L.;
RT "Mouse trp2, the homologue of the human trp2 pseudogene, encodes
RT mtrp2, a store depletion-activated capacitative Ca2+ entry channel."
RL Proc. Natl. Acad. Sci. U.S.A. 96:2060-2064(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RX PubMed=10998353;
RA Hofmann T., Schaefer M., Schultz G., Gudermann T.;
RT "Cloning, expression and subcellular localization of two novel splice
RT variants of mouse transient receptor potential channel 2."
RL Biochem. J. 351:115-122(2000).
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC -!- CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A

CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. MAY ALSO BE
CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=A;
CC Name=2; Synonyms=B;
CC Name=3; Synonyms=Alpha;
CC Name=4; Synonyms=Beta;
CC IsoId=Q9R244-1; Sequence=VSP_006562;
CC IsoId=Q9R244-2; Sequence=VSP_006564;
CC IsoId=Q9R244-3; Sequence=VSP_006565;
CC IsoId=Q9R244-4; Sequence=VSP_006566;
CC TISSUE SPECIFICITY: Isoform 3 is ubiquitously expressed at low
CC levels. Isoform 4 is expressed exclusively in vomeronasal organ.
CC -!- SIMILARITY: Belongs to the transient receptor family. StrpC
CC subfamily.
CC -!- SIMILARITY: Contains 3 ANK repeats.
CC -----
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CC -----
CC EMBL; AF111108; AAD17196.1; -
CC EMBL; AF111107; AAD17195.1; -
CC EMBL; AF230803; AAG29951.1; -
CC EMBL; AF230802; AAG29950.1; -
CC MGD; MGI:109527; Trpc2.
CC GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.
CC GO; GO:0000139; C:Golgi membrane; IDA.
CC GO; GO:0005635; C:nuclear membrane; IDA.
CC GO; GO:0015279; F:store-operated calcium ion concentration elevation; IDA.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; IDA.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR002111; Cat channel TrpL.
CC InterPro; IPR008979; Gal_bind like.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR005820; M_channel_nlg.
CC InterPro; IPR002153; Trans receptor.
CC InterPro; IPR005458; TRPChannel2.
CC InterPro; IPR002706; Xrcc1 N.
CC Pfam; PF00520; ion_trans.1.
CC Pfam; PF01834; XRCCL N.1.
CC PRINTS; PR01097; TRNSRCEPTRP.
CC PRINTS; PR01643; TRPCHANNEL2.
CC ProDom; PD023136; Xrcc1_N; 1.
CC SMART; SM00248; ANK; 2.
CC PROSITE; PS50088; ANK_REPEAT; FALSE NEG.
CC PROSITE; PS50297; ANK_REPEAT_REGION; FALSE NEG.
CC Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC ANK repeat; Repeat; Alternative splicing.
CC DOMAIN 1 659 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 660 680 POTENTIAL.
CC DOMAIN 681 702 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 703 723 POTENTIAL.
CC DOMAIN 724 738 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 739 759 POTENTIAL.
CC DOMAIN 760 789 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 790 810 POTENTIAL.
CC DOMAIN 811 833 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 834 854 POTENTIAL.
CC DOMAIN 855 899 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 900 920 POTENTIAL.
CC DOMAIN 921 1172 CYTOPLASMIC (POTENTIAL).
CC REPEAT 301 330 ANK 1.
CC REPEAT 377 406 ANK 2.
CC REPEAT 430 459 ANK 3.
CC DOMAIN 1140 1143 POLY-SER.

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 CC -----
 CC EMBL; AF054568; AAR00002.1; -;
 CC EMBL; AC005191; AAC24563.1; -;
 CC EMBL; AL049563; CAB44737.1; -;
 CC Genew; HGNC:12337; TRPCS.
 CC MIM; 300334; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0015279; F: store-operated calcium channel activity; TAS.
 CC GO; GO:0006816; P: calcium ion transport; TAS.
 CC GO; GO:0007399; P: neurogenesis; TAS.
 CC InterPro; IPR002110; Cat channel_TrpL.
 CC InterPro; IPR002111; Ion trans.
 CC InterPro; IPR005821; Ion trans.
 CC InterPro; IPR002153; Trans receptor.
 CC InterPro; IPR004729; Trp CaChannel.
 CC InterPro; IPR005451; TRPChannel5.
 CC Pfam; PF00023; ank; 2.
 CC Pfam; PF00520; ion trans; 1.
 CC PRINTS; PR01097; TRNSRECEPTR.
 CC PRINTS; PR01646; TRPCHANNEL5.
 CC SMART; SM00248; ANK; 2.
 CC TIGRFAMs; TIGR00870; ttp; 1.
 CC PROSITE; PS00088; ANK_REPEAT; FALSE NEG.
 CC PROSITE; PS02097; ANK_REPEAT_REGION; FALSE NEG.
 CC Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW ANK repeat; Repeat; Glycoprotein.
 FT DOMAIN 1 330 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 331 351
 FT DOMAIN 352 398 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 399 419 POTENTIAL.
 FT DOMAIN 420 437 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 438 458 POTENTIAL.
 FT DOMAIN 459 470 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 471 491 POTENTIAL.
 FT DOMAIN 492 512 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 513 533 POTENTIAL.
 FT DOMAIN 534 603 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 604 624 POTENTIAL.
 FT DOMAIN 625 973 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 69 98 ANK 1.
 FT REPEAT 141 170 ANK 2.
 FT SITE 971 973
 FT CARBOHYD 461 461
 FT SEQUENCE 973 AA; 111411 MW; FBC8CBF17BE42166 CRC64;
 SQ
 Query Match 4.1%; Score 247; DB 1; Length 973;
 Best Local Similarity 21.8%; Pred. No. 1.3e-08;
 Matches 143; Conservative 93; Mismatches 229; Indels 190; Gaps 27;
 QY 555 LKMSHLETEAARATREAKYERLALDLFSECYSSEARAFALLVERN-----RCW 606
 DB 227 LKLSKVENEFKAYEELSQCKLFAKLLDQARSRELE--IILNHRDDHSEELDPQKY 284
 QY 607 SKTCTLHLATEADAKAFHAGDGVQAFLTRIWGDMAGTPT-----ILRLIG----AFL 655
 DB 285 HDLAKLVAIKVHQEFVAPQNCQQLLATLWYD---GFPGRWRKHVVVKKLLTCMTIGFL 340
 QY 656 CPALVYTNLITSEAPLRTGLDLDLSLDTKSPLYGLQSRVEELVEAPRAQDGRGP 715
 DB 341 FPMLSLAYLIS-----P 352
 QY 716 RAVFLLTRWRKFWGAPVTVFLGNVWVYAFLLFLF---TYVLVDFRPPPPQSGSDEVIL 771
 DB 353 RSNLGL-----FIKKPFPIKCHTASVLTFLFLLASQHVIRTDLHVQGPPTVVEWMI 407
 QY 772 YFWVFTLVLEIRQ---GFTDEBTHLVKKFTLYVGDWNWKNCDMVAIFLFIIVGVTCEMLP 828

RESULT 9

TRPS5_RABIT

ID TRPS5_RABIT STANDARD; PRT; 974 AA.
 AC 062852;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Short transient receptor potential channel 5 (TrpCs) (Rtrps)
 DE (Capacitative calcium entry channel 2) (CCE2).
 GN TRPCS OR TRPS.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=98353453; PubMed=9687496;
 RA Philipp S., Hambrecht J., Braslavski L., Schroth G., Freichel M.,
 RA Murakami M., Cavalie A., Flockerzi V.;
 RA "A novel capacitative calcium entry channel expressed in excitable
 cells.";
 RT EMBO J. 17:4274-4282 (1998).
 RL
 CC -! FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
 CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY
 CC INTRACELLULAR CALCIUM STORE DEPLETION.
 CC -! SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
 CC -! SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -! TISSUE SPECIFICITY: Expressed predominantly in brain.
 CC -! SIMILARITY: Belongs to the transient receptor family. STpC
 CC subfamily.
 CC -! SIMILARITY: Contains 2 ANK repeats.
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 CC -----
 CC EMBL; AJ006203; CAA06911.1; -;

Db 408 LPWVLGFIWGEIEMMDGGFTE-----YIHDWNLMDFAMNSLIATISLIVA 456
 QY 829 SAFEAG-----RTVLAMDFWFTLRILHIFAIHKQLGPKIIVVERMKD 872
 Db 457 YVKNGSRPREWEMWHPITLAEALFAISNLISLISLFTANSGLPLQISLGRMLLD 516
 QY 873 VFFFLFSLVNLVAYG-----VTQALLHPH-----DGRLEWIFRVLVYP 913
 Db 517 ILKFLFYCLVLLAFANGLNQLFYFYETRAIDENCKGIRCEKQNNAFSTLP-ETLQSL 575
 QY 914 YLQIFGQIPIDEID-EARVNCSTHPLLEDSPSCPSLYANWLVILLVTLVTLVNLMLN 972
 Db 576 FWSYFGLNLVYTNVKAR-----HE-----FTEFVGATMGTNYNIVLSVLLN 618
 QY 973 LLIAFSTYTOVQGNADMFWKFORYNLIVEY-HERPALAPFP-ILLSHLS-LTLRRVFX 1029
 Db 619 MLIAMNNSQLIADHADIEWKPARTKLMSYFDEGGTLPPFNIIPSPKSFYLGWNFN 678
 QY 1030 KEAEHKREHLERLDPDLPDQKVTVTQVKNFSLKMEKRDS-----EGEVLKRTAH 1083
 Db 679 NTFCKRD-----PDGR-----RRRNLRSEFTERNADSLIQNHQYQEVIRNLVK 722
 QY 1084 RVDRIA-----KYLGLRGEQ-KRIKCLBSQINVCVSVSVSVADVLAQGGGPRS 1131
 Db 723 R--YVAAMIRNSKTHEGLTEENFKELKODISFRY-----EVLDLGNRKHPRS 769


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CC subfamily.
CC -!- SIMILARITY: Contains 2 ANK repeats.
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CC -----
DR EMBL; X99792; CAA68125.1; -.
DR EMBL; AJ224862; CAA12161.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR002153; Trans_receptor.
DR InterPro; IPR004729; Trp_CaChannel.
DR InterPro; IPR005460; TRPChannel4.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF0520; ion_trans; 1.
DR PRINTS; PR01097; TENSRECEPTP.
DR PRINTS; PR01645; TRPCHANNEL4.
DR SMART; SM00248; ANK; 2.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK_REPEAT; 1.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 331 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 332 352 POTENTIAL.
FT DOMAIN 353 364 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 365 385 POTENTIAL.
FT DOMAIN 386 438 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT DOMAIN 460 471 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 472 492 POTENTIAL.
FT DOMAIN 493 513 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 514 534 POTENTIAL.
FT DOMAIN 535 601 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 602 622 POTENTIAL.
FT DOMAIN 623 981 CYTOPLASMIC (POTENTIAL).
FT REPEAT 71 100 ANK 1.
FT REPEAT 143 172 ANK 2.
FT DOMAIN 617 981 BINDS TO ITPR1, ITPR2 AND ITPR3
(BY SIMILARITY).
FT SITE 979 981 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
(BY SIMILARITY).
FT VARSPLIC 1 513 Missing (in isoform Beta).
FT /FTID=VSP 006566.
SQ SEQUENCE 981 AA; 112531 MW; 57B172FD65B791C9 CRC64;

Query Match
Best Local Similarity 3.7%; Score 226; DB 1; Length 981;
Matches 153; Conservative 106; Mismatches 244; Indels 274; Gaps 31;

QY 555 LKEMSHLETE--AEARATREAKYERLALDLFSECVSNSEARAF-----ALLVRRNC 605
D 229 LQELSKVENEFSEVEELSRQCK--QFAXDLDDQTRSSRELIILNYRDNLSL--EEGS 284

QY 606 WSKTTCLEHLATADAKAFPHDGVQAFLETRIWWGDMA-----AGTPILRLGLAFCLCPA 658
D 285 GNDLARKLKAIRYQKEFVAQPCQLLASRWYDEFFGWRHWAQKMTVCIFVGLFPV 344

QY 659 LVYTNLITFSEAPLRTGLEDLQDLSLDEKSPYGLQSRVEELVEAPRAGQDRGPRV 718
D 345 FSVCVLI-----AP-----KSPIL-GL----- 359

QY 719 FLITRWKFWGAPVTIVLGNVVMYFAFLFTYVLL-----VDPRPQSGSPGV 769
D 360 -----FIRPFYKFICTASYLTFLFL-----LLLASQHDRSDLNROGPP--PTIVEM 406

QY 770 TLYFWVFTLVLEIRQ---GFTTDETHLVKXFTLYVGNWNKCDMVAIFLFIIVGVTCSM 826

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Db 407 MILPWVLGFIWGEIQKMDGGLOD-----YIHDWNLMDFMVMSLVATLSLKI 455
QY 827 LP-----SAFE-----AGTVLAMDPMVTLRLIHLIHAHKQLGPKLIIVVERMM 870
Db 456 VAFVKYSALNPRESMDMHPHTLVAEALFAIANIFSLRLISLFTANSHLGLPQLISGRML 515
QY 871 KDVFVFFLFLSVMLVAY-----GVTTQAL-LPHDGRLEWIFRRVLYRPV 914
Db 516 LDILAFLEFYCLVILAFANGLNQLFYEEYETKGLSCKGIRCEKQNNAFSTLP-ETQLSLF 574
QY 915 LQIFGQIFLDEIDAEARVNCSTHPLLEDSPSCPSLYANMLVILLAVTLFLLVNTVLMNLL 974
Db 575 WSIIFGLN-----LVVTNVKAQHEFTFVGATMTFTYNNVISLVLLNML 618
QY 975 IAMFSYTFQVVOGNADMFWKFORYNLIVEYHERPALAP-PFILL-----SH 1019
Db 619 IAMMNSYQLIADHADIEMKFARTKLMWSYFEGGTLPTFPNVIPSPKSLAWLIKWIWTH 678
QY 1020 L-SLTLR-----VFKEAEH-KREHLERDLPLDOKV-----TWETVOKENF 1062
Db 679 LCKKVRKXKPSFGTIGRRAADNLRHHQYQEWMLVKRYVAAMTRDAKTEGLTEFP 738
QY 1063 -----LSKMEK-----RRRDEG----- 1075
Db 739 KELQDISFRFVGLLGRGSLSTVQSAQGTKESSNSADSDEKSDNEGSKDKKNFSL 798
QY 1076 -----EVLRTAHRVDFA--KYLGGUREQEKRIK 1103
Db 799 FDLTLIHRSAIAAERHTISNGSALVQVEPREKQKRVNFTDIRHGLFHRRSKQHA 858
QY 1104 CLESQINVCSLVSSVADVLAQCGGPRSQ-----HCGEGSQLVAADR 1147
Db 859 AAEQANQIFSVSGVARQQAEGPLERSIQLSRTLASRGDLNIPGLSEQCILVDHR 915

RESULT 14
TRP4 HUMAN
ID TRP4 HUMAN STANDARD; PRT: 977 AA.
AC Q9UBN4; Q15721; Q9UBI0; Q9UBI1; Q9UBI2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Short transient receptor potential channel 4 (TrpC4) (trp-related
protein 4) (hTrp4).
GN TRPC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Kidney;
RX MEDLINE=20498755; PubMed=11042129;
RA McKay R.R., Symeczek-Seay C.L., Lievremon J.-P., Bird G.S., Zitt C.,
RA Juengling E., Lueckhoff A., Putney J.W. Jr.;
RT "Cloning and expression of the human transient receptor potential 4
(TRP4) gene: localization and functional expression of human TRP4 and
TRP3.";
RL Biochem. J. 351:735-746 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; DELTA AND GAMMA).
RC TISSUE=Embryonic kidney;
RX MEDLINE=21099836; PubMed=11163362;
RA Mery L., Magnino F., Schmidt K., Krause K.-H., Dufour J.-F.;
RT "Alternative splice variants of hTrp4 differentially interact with the
C-terminal portion of the inositol 1,4,5-trisphosphate receptors.";
RL FEBS Lett. 487:377-383 (2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=21671347; PubMed=11713258;
RA Schaefer M., Plant T.D., Stresow N., Albrecht N., Schultz G.;
RT "Functional differences between TRPC4 splice variants.";

```


QY 1063 -----LSKMEK-----RRDSEG----- 1075
 Db 737 KELKQDISSFRFEVLGLLRSSKLSITQSNASKSSNSADSDSEKSDSEGNKDKKNFSL 796
 QY 1076 -----EVURKTAHRVDFTAKYLG-GLRQEKRIKC 1104
 Db 797 FDLTTLIHPRSAIAISERHNISNGSALVQEPREKQKVFVTDIKNFGLFHRRSKQNA 856
 QY 1105 LESQINCVSLVSSVADVLA--QGGGP--RSSQHCGE-----SOLVAADHR 1147
 Db 857 AEQNAQ-----IFSVSEVARQAAGPLERNIQLESGLASRGDLIPGLSEOCVLVDHR 912

RESULT 15
 TRP4 MOUSE
 ID TRP4_MOUSE STANDARD; PRT; 974 AA.
 AC Q9QU05; Q62350; Q9QU09; Q9QZC0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short transient receptor potential channel 4 (TrpC4) (Receptor-
 activated cation channel TRP4) (Capacitative calcium entry channel
 TRP4). OR TRRP4.
 GN Mus musculus (Mouse).
 OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Brain;
 RA Zhu X., Boulay G., Jiang M., Birnbaumer L.;
 RT "Trp4 is involved in capacitative calcium entry in murine cells.";
 RN Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Brain;
 RA Qian F., Philipson L.H.;
 RN Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Brain;
 RX MEDLINE=98171352; PubMed=9512398;
 RA Mori Y., Takada N., Okada T., Wakamori M., Imoto K., Wanifuchi H.,
 RA Oka H., Oba A., Ikenaka K., Kurosaki T.;
 RT "Differential distribution of TRP Ca2+ channel isoforms in mouse
 brain.";
 RL NeuroReport 9:507-515(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=20545496; PubMed=10980202;
 RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V.,
 RA Zhu M.X.;
 RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ
 domain-containing protein, NHERF.";
 RL J. Biol. Chem. 275:37559-37564(2000).
 RN [5]
 RP SEQUENCE OF 505-642 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96003894; PubMed=7575478;
 RA Petersen C.C.H., Berridge M.J., Borgee M.F., Bennett D.L.;
 RT "Putative capacitative calcium entry channels: expression of
 RT Drosophila trp and evidence for the existence of vertebrate
 RT homologues.";
 RL Biochem. J. 311:41-44(1995).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=21113116; PubMed=11175743;
 RA Freichel M., Suh S.H., Pfeifer A., Schweig U., Trost C.,
 RA Weissgerber P., Biel M., Philipp S., Freise D., Droogmans G.,
 RA Hofmann F., Flockerzi V., Nilius B.;
 RT "Lack of an endothelial store-operated Ca2+ current impairs
 RT agonist-dependent vasorelaxation in TRP4-/- mice.";
 RL Nat. Cell Biol. 3:121-127(2001).

CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
 CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION. TRPC4
 CC DEFICIENT MICE LACK A STORE-OPERATED CALCIUM ENTRY IN ENDOTHELIAL
 CC CELLS.
 CC -!- SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES WITH
 CC INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR) (BY SIMILARITY).
 CC INTERACTS WITH NHERF.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=Q9QU05-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9QU05-2; Sequence=VSP_006570;
 CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN (HIPPOCAMPAL CA1
 CC PYRAMIDAL NEURONS, DENTATE GYRUS GRANULE CELLS, AND CEREBRAL
 CC CORTICAL NEURONS, AND IN THE SEPTAL NUCLEI AND THE MITRAL LAYER OF
 CC OLFACTORY BULB). LOWER LEVELS ARE DETECTED IN OTHER TISSUES.
 CC -!- SIMILARITY: Belongs to the transient receptor family. StrpC
 CC subfamily.
 CC -!- SIMILARITY: Contains 2 ANK repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF011543; AAD10167.1; -;
 DR EMBL; U50922; AAC05179.1; -;
 DR EMBL; AF190646; AAF01469.1; -;
 DR EMBL; U50921; AAC05178.1; -;
 DR EMBL; AF019663; AAD10168.1; -;
 DR EMBL; X90697; CA62230.1; -;
 DR PIR; S59128; S59128.
 DR MGD; MGI:109525; Trpc4.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR002153; Trans_receptor.
 DR InterPro; IPR004729; Trp_CaChannel.
 DR InterPro; IPR005460; TrpChannel4.
 DR Pfam; PF00023; ank; 2.
 DR PRINTS; PR01097; TENSRECEPTP.
 DR PRINTS; PR01645; TRPCHANNEL4.
 DR SMART; SM00248; ANK; 2.
 DR TIGRFAM5; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT; 1.
 DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
 DR ANK repeat; Repeat; Alternative splicing.
 KW DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 330 350 POTENTIAL.
 FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 363 383 POTENTIAL.
 FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 437 457 POTENTIAL.
 FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 470 490 POTENTIAL.
 FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 512 532 POTENTIAL.
 FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 600 620 POTENTIAL.
 FT DOMAIN 621 974 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 69 98 ANK 1.
 FT REPEAT 141 170 ANK 2.

Search completed: September 14, 2004, 00:04:52
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:02:13 ; Search time 26 Seconds

(without alignments)
4310.120 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence: 1 MQDVQPRPGSPGDAEDRE.....HRGLDGLWEQAGQPPSDT 1165

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:**

1: piri:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1134.5	18.6	488	JC7995	transient receptor
2	1070.5	17.6	1868	T23707	hypothetical prote
3	1000	16.4	1400	T22644	hypothetical prote
4	899	14.6	1707	T18951	hypothetical prote
5	326.5	5.4	1275	JU0092	trp protein - frui
6	317.5	5.2	1274	JN0015	trp protein - frui
7	294	4.8	1418	S40764	hypothetical prote
8	266.5	4.4	1124	JH0588	calmodulin-binding
9	247	4.1	999	F88391	protein R06B10.4 [
10	235.5	3.9	823	S44873	ZC21.2 protein - C
11	192	3.2	828	JC5807	trp3 protein - rat
12	176.5	2.9	793	S68238	trp-1 protein - hu
13	176.5	2.9	810	T38361	TRPC1 protein - hu
14	165	2.7	823	T34472	hypothetical prote
15	164.5	2.7	3678	S28916	dystrophin - mouse
16	160.5	2.6	482	S61648	probable membrane
17	146	2.4	725	JC7531	calcium transport
18	145.5	2.4	675	T20822	hypothetical prote
19	144.5	2.4	839	JC7621	capsaicin receptor
20	139	2.3	727	JC7796	epithelial calcium
21	132	2.2	790	T20312	hypothetical prote
22	130	2.1	838	T09054	hypothetical prote
23	130	2.1	2049	T43161	sodium channel pro
24	128	2.1	723	JC7795	epithelial calcium
25	128	2.1	900	T23026	hypothetical prote
26	124.5	2.0	608	G02640	polycystic kidney
27	123.5	2.0	1199	T37561	probable transcrip
28	123	2.0	1060	S63993	acrosomal protein
29	123	2.0	1075	T45570	kinesin-like prote

30	123	2.0	2019	2	A33996	sodium channel pro
31	122.5	2.0	2322	2	T10542	hypothetical prote
32	122.5	2.0	3685	1	A27605	dystrophin, muscle
33	121.5	2.0	2388	2	JE0271	beta spectrin, bet
34	121	2.0	937	2	T37241	olfactory channel
35	121	2.0	1657	2	T15838	hypothetical prote
36	120.5	2.0	854	2	T23155	probable non-ribos
37	120.5	2.0	854	2	T23155	hypothetical prote
38	120.5	2.0	1506	2	S52957	bimD protein - Eme
39	119	2.0	957	2	D88651	protein B0212.5 [1
40	118.5	1.9	2016	2	A38195	sodium channel pro
41	117.5	1.9	2472	2	A35715	fodrin alpha chain
42	116.5	1.9	1559	2	T30535	calcium channel al
43	116.5	1.9	1687	2	S41742	calcium channel al
44	116	1.9	149	2	S59129	trp-like protein -
45	116	1.9	638	2	JC7753	ring finger B-box

ALIGNMENTS

RESULT 1

JC7995

transient receptor potential-melastatin 4 channel - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003

C;Accession: JC7995

R;Murakami, M.; Xu, F.; Miyoshi, I.; Sato, E.; Ono, K.; Iijima, T.

Biochem. Biophys. Res. Commun. 307, 522-528, 2003

A;Title: Identification and characterization of the murine TRPM4 channel.

A;Reference number: JC7995; PMID:12893253

A;Accession: JC7995

A;Molecule type: DNA

A;Residues: 1-488 <NR>

A;Cross-references: GB:NM000319

A;Experimental source: Brain, C57/BL6

C;Comment: This protein, a member of subfamily of transient receptor potential channels,

C;Genetics:

A;Gene: trpm4

A;Map position: 7B2

A;Introns: 12/2; 153/2; 197/3; 256/1; 315/2; 384/1; 428/2; 452/3

C;Keywords: calcium entry; transient receptor potential; transmembrane domain; TRPM

Query Match	18.6%	Score 1134.5;	DB 2;	Length 488;
Best Local Similarity	47.6%;	Pred. No. 1.1e-74;		
Matches	236;	Conservative 72;	Mismatches 123;	Indels 65; Gaps 10;
QY	704	VEAPRAQGRGPRAVF--LLTRWRKFGAPVTVFLGNVVMYPAFLFETYVLLVDFRPP	760	
Db	20	VALERRQRRPGRALCCGKFSKRWSDFGAPVTAFILGNVSVLLFLLFAHVLVDFQPT	79	
QY	761	POGPGSPVTLVFWVFTLVLEIRQGF-----FTDEDTHLVKFTLVGVGNWVK	809	
Db	80	K-PSVSELLYFWAFTLLCEELQGLGGWGLASGGGRGDPRLRHLHLVLSDTNQ	137	
QY	810	CDMVAFLFIVGTCRMLPSAFEAGRTVLAMPFWFTLRIHFAHKGKPKIIVVERM	869	
Db	138	CDLLAITCELVGGGCRNTPGLDGLRTVLCCLDFMLFTLRLLHLFTVNGKQGPVIVSKM	197	
QY	870	MKDVFFFFLSVLVAYGVTTQALHPHDGRLDWIFRRVLXRPYLIQIFGQPLDIDEA	929	
Db	198	MKDVFFFFLSVLVAYGVATEGILRPQDRSLPSILRRVFRYPYLIQIFGQIPQEMDVA	257	
QY	930	RV-----NCS-----THPLLEDSP---SCPSIYANWLVLVLLVTLVTVNLLMLLIAM	977	
Db	258	LMIPGNCMERGSWAHP-----EGPVAGSCVSYANWLVLVLLVTLVTVNLLMLLIAM	313	
QY	978	FSYTFQVVGNDMFWKFORYNLIYVEHERPALAPPFILLSHLSLTLR-----RVFK	1029	
Db	314	FSYTSKVHGNSDLTWKAQRYSLIREHSRPAAPLIITISHVRLDLMWRRCRRRAN	373	
QY	1030	KEAEKREHLERDLPDLDQKVVTWETQKFNFLSKMEKRRRDSGEVLKTAHRVDFIA	1089	

Db 374 LPASPVFEHFRVCLSKAERKLLTWESVHKENFLAQAQRKSDSERLKRKTSQKVDTAL 433
 Qy 1090 KYLGLEOEKRIKLESIQINVCVSVLSSVADVLAAQGGPRSSQHCGBGSQSLVAADHRGG 1149
 Db 434 KQLQIRYDRRLGLEVEVHCRLVTWBAALSH-----SALL----- 473
 Qy 1150 LDGWEQPGAGQPPSDT 1165
 Db 474 -----PPGAPPPPSPT 484

RESULT 2
 T23707
 hypothetical protein T01H8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T23707; T24342
 R:Kershaw, J.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19786
 A:Accession: T23707
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1868 <W1L>
 A:Cross-references: EMBL:Z83117; PIDN: CAB05572.1; GSPDB: GN00019; CESP: T01H8.5
 A:Experimental source: clone M04C7
 R:Lennard, N.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19877
 A:Accession: T24342
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1868 <W12>
 A:Cross-references: EMBL:Z80219; PIDN: CAB02303.1; GSPDB: GN00019; CESP: T01H8.5
 A:Experimental source: clone T01H8
 C:Genetics:
 A:Gene: CESP: T01H8.5
 A:Map position: 1
 A:Introns: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1

Query Match 17.6%; Score 1070.5; DB 2; Length 1868;
 Best Local Similarity 24.5%; Pred. No. 3.9e-69;
 Matches 343; Conservative 231; Mismatches 486; Indels 341; Gaps 41;

Qy 26 GEVNP-GSGKRGKRFVPSGLVFLDILAEWHLPAPNLVSVLGGEGEPPFAMKSWL 84
 Db 214 GQVEFGGPHPYKAYVRNFTPEYIMSLFEHWQISPPRLIITVHGTSNFDLPKL 273
 Qy 85 RDVLRKGLVKAQAGTAMLTSLARVGLARHVGQAVRDHSLASTSTKVRVAVAGVASLGR 144
 Db 274 ARVFRKGLLKAATTCAMITISGCDTGVVKKHVAALLEG---AQAQRNKIVGIGIAPWG- 329
 Qy 145 VLHRRILEAEADF-----PVHYEDDGGSGPLCLSDSNLSHFILVEPFGPGKDGIL 198
 Db 330 -----LUKREDFITGQDKTVYP-----SSSGRTGLNNRHSYFLLVDNGTVGRYGA 380
 Qy 199 ELRLREKHISQRAQYGTGIEIPVLCLVNGDPNTERISRAVEQA--APWLILYGS 256
 Db 381 ILRKLWYISQKIFGTR--VPVVCVLEGGSTIRSVLDVTNVPRVPVVCVCGS 438
 Qy 257 GGIAVDLAAL-----VNPHLL-----VPKVAEKOFKFPKPHFSWEDIVRTWTKLONI 306
 Db 439 GRAADLLAFHQNVTEGGLPDIRQVRLVLTFTFGSEAAH-----RLHLEL 488
 Qy 307 T---SHQHLTVDYDPEQGSBELDTVLKALVKACKSHSQBPQDYLDELKLAVALVDV 363
 Db 489 TVCAQKRLITIFRLGEQGEHVDHALTALKG-----QNLSDAQALALANRVDI 542
 Qy 364 AKSEIFNGDVEMKCDLEEVMDALVSNKPEFVRLFDVNGADVADFLTVGRLELY---- 419
 Db 543 ARSDVFMGHEWFPQAALHNAMWALHTRDVFRLLEQGINNQKFLATSLRDELNYTDK 602
 Qy 420 -----RSVSRK-----SLFLDLL-----QRKQEAL- 441

Db 603 GPPNTLFYIVRQVVRVQGYRFLKPLDITGLVIEKLMGNSYQCSYTTSEFRDYKORMKRVK 662
 Qy 442 -----TLAGLTQOARE-----PPAGPPA-F 461
 Db 663 HAQKAMGVSSRRSRPTGSGIASQSTEGMGVGGSSVAGVFGNSFGNQDPLDPHVR 722
 Qy 462 SLHEVSRVLKDFL--QDAGRFYQDGRPRRRRAEKGAKPPTQKWLILDLNOKSEN--- 516
 Db 723 SALSGSRALSNHILWRGAFRCNF---PANDMRPNLGDSDRCGSEFDEELSLTSASDGS 778
 Qy 517 -----PWEDLFLWAVLQNRHEMATYFWAMGQGVAAALAAKILKEMS-----HLE 562
 Db 779 QTEPDFRYPYSELMIWAVLTKRQDMAMCMWQHGEAMAKALVACRLYKSLATEAEDYLE 838
 Qy 563 TEAEARATREAKYERIALDLFCYCSYNSAEARAFALLVRRNRKWSKTKTCLHATEADAKA 622
 Db 839 VEICEELKYABEPRILSLELLDCHYHVDDAQTQLLTLYELSNWSNEICLALAVIVNNKH 898
 Qy 623 FFAHDGVQAFLTRIWDGMAAGT--PIRLRLGAFICPALIV----- 660
 Db 899 FLAHPCCQIILLADLWHGGLRMRTHSNIKVVLGLICPPFIOMLEFKTREELNQPTQAAEH 958
 Qy 661 -----YTNLITFSEAPLRTGLELDQLDLSLDT----- 689
 Db 959 QNDMNYSS 1018
 Qy 690 ----- 689
 Db 1019 LFHSRRKAKKNEKCDRETDSACEAGNRQIQNGGLTAETGTFGESNGVSPPPYMRANS 1078
 Qy 690 -----KSPLYGLOSVEELVEAPQAQDR-----GPAVFLLTRWRKFW 728
 Db 1079 RSYNNRSDMSKTSVIFGSDPNLSKLOKSNITSDRPNMPEQFGTKIKMRFRYEFY 1138
 Qy 729 GAPVTFLGNVVMYFAFLFETVYLLVDPRPGPSGPEVTLFVFWVTLVELEIRQGF 788
 Db 1139 SAPISTFMSWTISFILFTFTFTYLLV--KTPPR-PTVIEYLIAVAAFGLEQVKRLIM 1195
 Qy 789 TDETHLVKTKTLVVGDNWKNKCDVVAIFLFTVGTCTMLPSAFAGRTVLAMDFMVFILR 848
 Db 1196 SDAPK-FYEKIRTYVCSFNNCVTILAIIFYIVGFMRFCGVS-AYGRVILACDSVLWTWK 1253
 Qy 849 LIHFAIHQKQKPKIIVVERMMKOVFPFLFSLVWLVAVGTQTQALLHPHGRLEWIP-R 907
 Db 1254 LLDYMSVHPKLGYPYTMAGKMIQNSYIIVMLVLTLSFGLARQSIYTP-DETWHILVR 1312
 Qy 908 RVLVRPYLQIFGOPLDEIDEARVNCSTH-----PLLEDSP---SCPSLYANWL 954
 Db 1313 NIFUKPYFMYGEVVADEID---TCGEANDQHLNGPVLGNGTGLSCVPQY--WI 1366
 Qy 955 VILLVTLVTLVNLVLLNLLIAMFSYTFQVVGADMEFKQRYNLIVYEHHERPALAPPF 1014
 Db 1367 PPLMTFFELLIANILLMSMLIAFNHIFDADENKQIWLFRQYKQVMEYSTPLPPLP 1426
 Qy 1015 ILLSHLSUTLRRVFKKEAEHKEH-----LERDLPDLDDQKVTWETVQKENFL-S 1064
 Db 1427 TPLVHGVILQIFVTRLSKCSQERNPILLKIAELFLDNDQIEKHLFEEDCMEDLARQ 1486
 Qy 1065 KMEKERRDSEGEVLKRTAHR-----VDFIAKYLGG---LREQEKRIKCLQSINYCSV 1114
 Db 1487 KLNKNTNEORILRADIRTDQILNRLDLQAKESMGDRVDINDVESRLASVEKAQN---E 1543
 Qy 1115 LVSSVADVLAAQGGPRSSQHC 1135
 Db 1544 ILECVALLNQNNAPTAIGRC 1564

RESULT 3
 T22644
 hypothetical protein F54D1.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:\Accession: T22644
R:Lennard, N.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19592
A:Accession: T22644
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1400 <WIL>
A:Cross-references: EMBL:Z77132; PIDN:CAB00861.1; GSPDB:GN00022; CESP:F54D1.5
A:Experimental source: clone F54D1
C:Genetics:
A:Gene: CESP:F54D1.5
A:Map position: 4
A:Introns: 21/2; 51/2; 205/2; 276/3; 364/2; 466/3; 507/3; 536/3; 599/3; 672/2; 699/3

Query Match 16.4%; Score 1000; DB 2; Length 1400;
Best Local Similarity 27.8%; Pred. No. 3.5e-64;
Matches 335; Conservative 204; Mismatches 478; Indels 188; Gaps 46;

QY 26 GEVNF-GSGKRGKRVFVPSGVAPSVLFDLLAEWHLPAPNLVSLVSGEEQPFAMKSWL 84
DB 151 GTIVQGGHAHAQAQVRLSYDSEPLDVYMLKEVWGLEAPRLVITVHGMNFEELEEL 210
QY 85 RDVLRKGLVKAQOSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKVRVAVGMASLGR 144
DB 211 GRLFRKGLKAAQTGGAWIITSGLDGSGVVRHAKAL-DEAGISARRMSQIVTIGIAPWGV 269
QY 145 VLHRLILEAQEDFPVHYPEDDGGSGPLCSLDNSLSHEILVPEPPGKGDGTELRLRL 204
DB 270 IRRKRLIRONEH--YYVDHSLSVNANVGIILDRHSYFLLADNGTVGRFGADLHLRQNL 327
QY 205 EKHISEQRAGYGGTGTIEIPLVCLLVNGDPNTERISRAV--EQAAPWLILVSGGIADV 262
DB 328 ENHI-----ATFGNGR-KVPVVCTILLEGISINAHIDVYTMKPDIPALVCDGSGRAADI 382
QY 263 L---AALVNQPHLLVPKVAEK--OPKEKPPSKHFSWEDIVRWTKLQNLITSHQHLTVY 316
DB 383 ISFAARYINSDGTFAAEVGEKRLNLIKWFVPET--DQEMFR-KITECVI-RDILLRIF 437
QY 317 DFEQSGSELDVILKALVKACKSHSQEPQDYLDELKAVANDRVDIKSEIFENGVEWK 376
DB 438 RYQGEEDVDVFLITVLQ---KQNLPPD--EQALTLISNVRDLAKSLFSGNRKWS 491
QY 377 SCDLSEVMVDALVSNKPEFVRVFDNGADVFLTYGRLOELY-----RSVSRKSL 428
DB 492 SDVLEKANDALYWDVDFVECLLENGVSKNFSLINRLENLYNMDIDINSAHSVRNWMEN 551
QY 429 FDLQRKQBEARLTLAGLTOQAREPPGAPFAPSLHEVSRLVKDFLQDACRGFYQDGRPG 488
DB 552 FDSM--DPHTVLTIPMG-QVVEKLMG-NAFQLYTTSSEFK-----GKYD 592
QY 489 DRRRAEKGK--AKRPTGOKWLL-----DLNQSEN-----PWRDLFLMAVLQNRHEM 533
DB 593 RYKRINQSSYFHRKRVKIVQELFKKSDQDQINDNEEDFSFAYPFNDLLIIMAVLTSRHM 652
QY 534 ATYFWAMGQGVAAALAAKILK-----EMSHLETEAEARATREA-KYERLALDLFSE 586
DB 653 AECMWVHGEDAMAKCLLALRYLKATAKIAEDYLDVE-EAKRLFONAVKCREDAIELLDQ 711
QY 587 CYSNSEARAFALLVRNRNCRWSTKTCCLHATEADAKAFFAHGQVQAFELTRIMWGM--AAG 644
DB 712 CYRADHRTLRLRLMELPMWGNCLSLAVANTKTFLAHPCCQILLAEHLHGSLKVRSG 771
QY 645 TPILRLIGAFIC-PALVY-----TNLITSEAPLTGLIEDL-QDLDSLDLTKESPLY 694
DB 772 SNV-RVLTALICPPALIFMAYKPKHSKTLRLSEETP-----EQLPYPRISITTSNRY 825
QY 695 GLQSRVEELVEAPRAOG-----DRCPRAVE-----LLTRWPK 726
DB 826 RYSGKEEQKEKTELLEKSTYKVTIISRRKNSGVASVYGSASMMKRPQNLKPFERFA 885
QY 727 FMGAPVTVFLGNVVMYFAFLFLTYVLLVDPRPPPGQSGPEVTLTFYVFTLVLEIROG 786
DB 941

886 FYSSPITRFSWSCI AFLIFLTQTICILLLE---TSLKPSKYEWITFTVTVLSVEHIRK- 941
QY 787 FETDEDTHLVKKFTLYVGDNNKCDMVALFPIVGTCTRMPLSAFEA-GRTVLAMDPMVF 845
DB 942 LMTSEGRINEKRVYAKWYNITWSAALLPFLVGGFRLVPMYRHSWGRVLLSPSNVLF 1001
QY 846 TURLJHIFAIHQKQPKIIVVERMMKDVFFFLFSLVMLVAYGVTTQALLHHPDHGLEWI 905
DB 1002 YMKIFEYLSVHPLGPIQMAKWSXCYICVLLVPLMAFGVNRQALTEPNVKDWHML 1061
QY 906 F-RVLYRPIYQIFQOIPDEIDEARVNCSTHPLLEDSPPSCPSLYANWLVILLVTFLL 964
DB 1062 LVNRNIFYKPYFMYGEVAGEID---TCG-----DEGIRCFPGY--PIPLLWVIFLL 1109
QY 965 VTNVLLMLLITAMESYTVQVQGNADMFWKFORNYLIVEYHERPALAPEILLSHL--- 1020
DB 1110 VANILLULLLITAFNNIYNDISIEKKEIWLFORYOQLMEYHDSPLPPFPSTFAHYHFI 1169
QY 1021 --SLTLRRVFKK-----EAEHKKR-EHLERDLPDQKVVWETVQKENFLS 1064
DB 1170 DYLYNLRPRDTKRFRSEHSIKLSVTEDEMKRQDFEEDCIDLTR-----IRK---L 1218
QY 1065 KMEKRRRSEGEVLKRTAHRV-----DPIAKYGLGLREQEKRIKLESQINVCVLSV 1118
DB 1219 KLNTKEPLSVTDLTBLTCQVRHDLMQENFLK-----SRVYDIETKIDHISNSDE 1269
QY 1119 VADV 1123
DB 1270 VVQIL 1274

RESULT 4
T18951
hypothetical protein C05C12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18951
R:White, S.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19050
A:Accession: T18951
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1707 <WIL>
A:Cross-references: EMBL:Z68333; PIDN:CAA92726.1; GSPDB:GN00022; CESP:C05C12.3
A:Experimental source: clone C05C12
C:Genetics:
A:Gene: CESP:C05C12.3
A:Map position: 4
A:Introns: 13/3; 52/1; 82/3; 100/3; 174/3; 203/1; 249/2; 292/1; 358/2; 406/2; 436/2; 477/3; 542/3; 1595/1; 1647/2; 1673/3; 1695/3

Query Match 14.6%; Score 889; DB 2; Length 1707;
Best Local Similarity 22.3%; Pred. No. 6e-56;
Matches 308; Conservative 229; Mismatches 456; Indels 390; Gaps 43;

QY 26 GEVNF-GSGKRGKRVFVPSGVAPSVLFDLLAEWHLPAPNLVSLVSGEEQPFAMKSWL 85
DB 197 GNIVFEGTA-HHAQYARISFSDSDPRDIVLHMMKWKLPKPKLIITTINGLTKFDLPKLA 255
QY 86 DYLRKGLVKAQOSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKVRVAVGMASLGRV 145
DB 256 RFFRKGIMKIATKSTDAWIITSGLDGSGVVKHLDLSALHDH--GNHTSKNHVVAIGIASWGL 313
QY 146 LHRILEBAQEDFPVHYPEDDGGSGPLCSLDNSLSHEILVPEPPGKGDGTELRLRL 205
DB 314 KQRS--RFVGKDSVTYATNVFNNT-RLKELNDNHSYLFSDNGTVNRYGABIIIMRKLE 370
QY 206 KHISEQRAGYGGTGTIEIPLVCLLVNGDPNTERISRAVE--QAAPWLILVSGGIADV 263
DB 371 AVLAQ-----GDKKRSAPLVCVLEGGAFITKVMHVVYTTIPRIPVIVCDGSGRAADIL 425
QY 264 A-----ALVNQPHLLV---PKVAEQKFKFKFSKHSWEDIVRWTKL 302

Db 426 AFAHQAVSQNGFLSDNIRNQLVNI VRRIFGVDPKTAQKLIQ----- 467
Qy 303 LONITSHOHLTVYDFEGSEELDTVLKALVACKSHSQBPQDYLDLKLAVANDRVD 362
Db 468 IVECTNKSMTIFRLGSSREDLDHVMSCLL---KQNLSP---EQLQLALANRAD 521
Qy 363 IAKSEIFNGDVEWKSCLDEEVVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELY--- 419
Db 522 IARTEIFANGTEWTTQDLHNAMIBALSNDRIDFVHLLLENGVSMQKFLTYGRLEHLYNTD 581
Qy 420 ---RSVSRKSLFLDLLQKQBEARLTLAGLGTQQAAREPPGAPFAPSLHEVSRVLKDFLOD 476
Db 582 KGPQNTLRNLVDSKHH-----IKLVEVGRLEVENLMGN 615
Qy 477 ACRGFYQD-----GRPDGRRAEK----- 495
Db 616 LYKSNYTKBEFNQYFLPNRRKQFGRVHSNNGRNDVIGPSGDAGRSMSSQWLSLIN 675
Qy 496 -----GPAKPTGQKWLIDLNLQKSEN-----PWRDLFLWAVLQNRHEMATY 536
Db 676 NARNSIISLFGGGRKRESDEDDPSNLEEEANMDFTERYPYSDLMIAWVLTQKQMAKL 735
Qy 537 FWAMQOEVAAALACKILKEMSHLETEAARATREA-----KYERLALDLFS 585
Db 736 MWTHGEGGAKALVASRL-----YVSLAKTASLATGEICMSQDFTFEFSSELA VELE 790
Qy 586 ECVNSSEARAPALLVRRNRKSKTTCLHLATEADAKAFPAHDGVAQFLTRIWWGDMA--- 642
Db 791 YCTKHGRDQTLRLTCELANWGDETCLSLAANNHGRKFLAHPCCQMLLSDLWQGLLMKN 850
Qy 643 -AGTPILRLLAGFLCPALVYTNLTFFSEAPLR-----TG 676
Db 851 NQNSKVLTCCLAA---PPLIF--LLGFKTKEQLMLQPKTAAEHDEMSDSMNSAEDTDS 905
Qy 677 LEDQLDLSLTE-----KSPLYGLSRVEELVEA 706
Db 906 SDSSSDSDSDSEDAKLAQSLASADOPLSIHLVRDKLNFSEKKPDNG---ISRIVVA 961
Qy 707 P-----RAO----- 710
Db 962 PPVITGRNARTMSIKSKKNVKKPACLKLETSDDDEQOKKATEMCKSTFFDFDFP 1021
Qy 711 -----GDRGPRAV-----FLLTR-----WRK 726
Db 1022 YINRTGKGSVAVAMNHDDVIDPSEELDTQTRKSSREFSSRNVTQVYVTORELSWK 1081
Qy 727 ---FWGAPVTVFLGNVVMYFA---FLFTFYVLLVDFRPPPGSPGSEVTLYFWVFTLV 779
Db 1082 KIMBFYKAPITTYW---LWFFAFIWFLLTYNLVKTQ---RIASNSEWYVFAFYWT 1135
Qy 780 LE---EIRQGFDTEDTHLVKKFTLYVGDNNWKNCDMVAIFLFI VGTCTRMPLPSAFEAGRT 836
Db 1136 LEIGRKVVSTTMDTSKPVQLQVFPFQYRNGLLAFGLLYLIAYFIRLFTTKLGR 1195
Qy 837 VLAMDFWVFTLRLHIHFAHKOLGPKIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLH 896
Db 1196 LIICNSVILWSLKLVDYLSVQOGLGPIYINVAEMPTMPLCVLVPITLYAFGLLRQSTY 1255
Qy 897 PHDGRLEW---IFSRVLYRPYLIQFQIPLDEIARVNCSTHPLLLSDSPSCPSLYAN- 952
Db 1256 PYE---DWHVILVRNIFIQPFMLYGEVYAEID---TCGDEIWTQTHEDENIPISMLNV 1308
Qy 953 -----WLVIILLVFLVTVNLLNLIAMPSYTFQV---VQGNADMFWKFRYNLIV 1002
Db 1309 THETCVPGYWIAPVGLTVFMLATNVLNVMVAGCTYIFEXHIOSTRIF-LFERYGQVM 1367
Qy 1003 EYHERPALAPPFILLSHLSLTLRRVFKKEABHKREHL-ERDL-----PDLDQKVVTWET 1056
Db 1368 EYESTPWLPPPTTIYHVIWFLFKLISSSRMFERKNLFDQSLKFLSPDEN-EKVHTFEE 1426
Qy 1057 VQKNFLSKMKRRRDSGEVLRTAHRVDFTAKYLGGL-----REQEKRIKCL 1105

Db 1427 ESVEDMKRETKKNLSSNDRIRHTAERTDAILNARVSHLTQLEFTLKEEIRELEHKMKM 1486
Qy 1106 ESQ 1108
Db 1487 DSR 1489
RESULT 5
JU0092
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
C:Accession: JU0092
R:Montell, C.; Rubin, G.M.
Neuron 2, 1313-1323, 1989
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral membrane protein
A:Reference number: JU0092; MUID:90180449; PMID:2516726
A:Accession: JU0092
A:Molecule type: mRNA
A:Residues: 1-1275 <MON>
A:Experimental source: strain Oregon R
C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the photoreceptor
C:Genetics:
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
C:Superfamily: TRP3 protein
C:Keywords: transmembrane protein
F:334-354/Domain: transmembrane #status predicted <TM1>
F:378-401/Domain: transmembrane #status predicted <TM2>
F:419-436/Domain: transmembrane #status predicted <TM3>
F:457-471/Domain: transmembrane #status predicted <TM4>
F:504-527/Domain: transmembrane #status predicted <TM5>
F:612-630/Domain: transmembrane #status predicted <TM6>
F:636-661/Domain: transmembrane #status predicted <TM7>
Query Match 5.4%; Score 326.5; DB 2; Length 1275;
Best Local Similarity 20.3%; Pred. No. 4.3e-15;
Matches 178; Conservative 123; Mismatches 264; Indels 313; Gaps 37;
Qy 305 NITSHOHLTVYDFEGSEELDTVLKALVACKSHSQBPQDYLDLKLAVANDRVDIA 364
Db 86 NVILLEHIEVGDALLHAISEYVEAVEELLQWETHKEGQPY-----SWEAVDRS 137
Qy 365 KSEIFNGDVEWKSCLDEEVVMDALVSNKPEFVRLFDVNGA-----DV 406
Db 138 KS-FTVDI-----TPLILAAHNNYELIKILLDRGATLPMPHDVKCGCECVTSQT 188
Qy 407 ADFLTGRLQ-ELYRSVSRKSLFLDLLQKQBEARLTLAGLGTQQAAREPPGAPFAPSLH- 464
Db 189 TDSLRHSQSRLNAYRALSSALI-----ALSSRDPLV--TAFQLSW 227
Qy 465 EVSRVLKDFLODACRGFYQDGRPGDGRRAEKGPAKRP TGQKWLIDLNLQKSENPRDLFLW 524
Db 228 ELKRL--QAMESFEAEYTEMR---QMVQDFGTS-----LLDHARTS-----MELE 268
Qy 525 AVLQNRHMYATFWAMQOEVAAALACKILKEMSHLETEAARATREAKEYERLALDLF 584
Db 269 VMLNFNHPSHDIWCLGQ-----ROTLE----- 292
Qy 585 SECYSNSEARAFALLVRRNRKSKTTCLHLATEADAKAFPAHDGVAQFLTRIWWGDMAAG 644
Db 293 -----LKAIRYKQKTFVAHPNVQQLAAIWDY----G 321
Qy 645 TPILRLLAGFLCPALVYTNLTFFSEAPLRGTLEDQLDLSLDEKSPLYGLSRVEELV 704
Db 322 LPGR-----RKQASQQLMDVVKLG-C-SFPIYSL-----KYI 352
Qy 705 EAPRAQGRGRPRAVFLTLTRWKFVGPVTVFLGNVVMYFAFLFL----- 748
Db 353 LAPDSEG-----AKFMRKPFVKFITHSCSYNFFLMLLGAASLRVYQITFELL 399
Qy 749 -FTVVL--LVDFRPPQG--PSGPEVTLYFWVFTLVLEIR---QGFTEDETHLVKKF 799

Db 400 APPWMLTLEDRKHERGSLPGPIELAIITYIMALIFEELKSLYSGLFE----- 449

QY 800 TLYVGNWNNKDMVAIFLFIIVGVTCR-----MLPS 829

Db 450 --YIMDLNINVIDIISNMVFTWTLRCRATAWIVHRDLWFRGIDPYPRHWHPPDFDMLLS 507

QY 830 --AFAGRTVLAMDVFVT-LRLIHIFAIHQKGPKIIVVERMKDVFVFFFLSVMLVA 886

Db 508 EGAFRAG-----MVFSYLKLVHIFSINPHLGPQVSLGRMIIDIIKFFFIYTLVFA 559

QY 887 YGVTTQALL-----HPHGRLEW-----IFRRV--LYRP-----YLOIFGQ 920

Db 560 FGCLNQLLWYAELEKKNKYHLHPVADFDOQEKACTIWRFSNLFETSQSFLWASFLG 619

QY 921 IPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLVTLVTLNVLNLLIAMFSY 980

Db 620 VDLVSFDLAGIKS-----FTRFWALLMFGSYSVINIIVLLNMLLIAMNS 663

QY 981 TFQVQGNADMFMKFORYNLIVEYHE-RPALAPPFILLSHLSLTLRRVFKKAEHKREHL 1039

Db 664 SYQIISERADTENKFARSQWMSYFDDGTIPPPFNLCNPMKMLRKTGLGRKPSRTKSF 723

QY 1040 ERDL--PDLQXVVTWETVOKENFLSKMKRRDSEG 1075

Db 724 RKSMEQAOTLHDKVM--KLLVRYIT-AEQRRDDYG 757

RESULT 6

JN0015

trp protein - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001

C;Accession: JN0015

R;Wong, F.; Schaefer, E.L.; Roop, B.C.; LaMendola, J.N.; Johnson-Seaton, D.; Shao, D. Neuron 3, 81-94, 1989

A;Title: Proper function of the *Drosophila trp* gene product during pupal development is A;Reference number: JN0015; PMID:90148782; PMID:2482778

A;Accession: JN0015

A;Molecule type: mRNA

A;Residues: 1-1274 <WON>

C;Comment: This photoreceptor membrane-associated protein is not required for the occur

C;Genetics:

A;Gene: trp

A;Cross-references: FlyBase:FBgn0003861

A;Map position: 99C5-6

C;Superfamily: TRPC3 protein

C;Keywords: Glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane pro

F;1257-1263/Region: nucleotide-binding motif A (P-loop)

F;64,70,899/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted

F;800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 5.2%; Score 317.5; DB 2; Length 1274;

Best Local Similarity 20.3%; Pred. No. 2e-14;

Matches 187; Conservative 132; Mismatches 273; Indels 327; Gaps 41;

QY 274 VPKVAREK-QFKEKFPKSHFSWEDIVRWTKLQWITSH-----QHLLTVVDFPQEGS 323

Db 48 VKKILEYQGTDF--NINCTDPMNRSAISIENENFDMLVILHEHNEVGDALLHAI 104

QY 324 BELDTVLKALVKACKSHSQEPDYLDELKAVANDRVDIKSEIFNGDVEMKSCDLEEV 383

Db 105 SEYVEAVEBELLQWETNKEGQFY-----SWEAVDRSKS-TFTVDITF----- 147

QY 384 MVDALVSNKPEFVRLFDVNGA-----DVADFLYGLRQL-ELYRSVSR 424

Db 148 LILAAHNNYELIKLILDRGATLMPHDVKCGDECVTSQTQTDLSRHSQSRIINAYRALSA 207

QY 425 KSLIFDOLLQKQEARLTLAGLTQQAAREPPAGPPAFSLH-EVSRVLKDFLODACRFGYQ 483

Db 208 SSLI-----ALSRDVL--TAFQLSWEIKRL--QAMESFEAREYT 244

QY 484 DGRPGDRRAEKGPAPKPTGQKWLLDLNQSENPMRDLFIWAVLQNRHEMATYFWANGOE 543

Db 245 EMR---QMVDGCTS-----LLDHARTS-----MELEVMNFNHPSHDIW----- 282

QY 544 GVAALAAACKILKEMSHLETEAARATREAKYERIALDLDFSECYNSARAPALLVRN 603

Db 283 -----CLASSET-----LER-- 292

QY 604 RCWSKTTCLHLATEADAKAFFADHGVOAFLTRIWMGDMAAGTPIRLLLGALFLCPALVYTN 663

Db 293 -----LKLAIYKQKTFVAHPNVQQLAAIW-----YDG 321

QY 664 LITFSEAPLRTGLDQLDLSLTDEKSPLYGLQSRVBEVLAPRAQGRGPRAVFLTR 723

Db 322 LFGFQPEAS-----QQLMDVWKLGC-SFPIYSI--KVILAPDSEG----- 358

QY 724 WKFWGAPVTVFLGNVVMYFAFLF-----FTYVL--LVDRPPPPQG-- 763

Db 359 -AKFMRNPFLYSSSRTPCPSYMFLLMLLGAASLRVQITFELLAPFMMWLTWLEDWRKHERGS 417

QY 764 -PSGPEVTLYFWVFTLVLEEIR---QGFFTDEBTHLVKKFTLYVGDNNKNCIMVAIFLF 818

Db 418 LFGPIELAITIYIMALIFEELKSLYSGLFE-----YIMDLNINVIDIYSNMFY 465

QY 819 IVGVTCR-----MLPS--AFAGRTVLAMDVFVT 846

Db 466 VTWILCRATAWIVHRDLWFRGIDPYPRHWHPPDFDMLLSEGAFAG-----MVFS 517

QY 847 -LRLTHIFAIHQKGPKIIVVERMKDVFVFFFLSVMLVANVGVTTQALL----- 895

Db 518 YLKLWHIFSINPHLGPQVSLGRMIIDIIKFFFIYTLVLFAGCGNQLLWYAELEKKN 577

QY 896 --HPHDGRLEW-----IFRRV--LYRP-----YLOIFGQIPLDIDEARVNCSTHPLL 939

Db 578 CYHLHPDVADFDDQEKACTIWRFSNLFETSQSFLWASFLGLVLDVSFDLAGIKS----- 631

QY 940 LEDSPSCPSLYANWLVILLVTLVTLNVLNMLLIAMFSYTFQVQGNADMFMKFORYN 999

Db 632 -----FTRFWALLMFGSYSVINIIVLLNMLLIAMNSYQIISERADTENKFARSQ 681

QY 1000 LIVEYHE-RPALAPPFILLSHLSLTLRRVFKKAEHKREHLERDL--PDLQXVVTWET 1056

Db 682 LMSYFDDGTIPPPFNLCNPMKMLRKTGLGRKPSRTKSFMRKSMERAQTLHDKVM--K 738

QY 1057 VQKENFLSKMKRRRDEG 1075

Db 739 LILVRYIT-AEQRRDDYG 756

RESULT 7

S40764

hypothetical protein ZK512.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Nov-1999

C;Accession: S40764

R;Hawkins, T.; Ainscough, R. submitted to the EMBL Data Library, February 1993

A;Reference number: S40759

A;Accession: S40764

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1418 <HAW>

A;Cross-references: EMBL:Z22177; NID:g297989; PID:g297992

C;Genetics:

A;Introns: 199/1; 238/1; 290/2; 529/3; 557/3; 588/3; 677/2; 733/3; 772/3; 846/3; 946/1;

C;Superfamily: *Caenorhabditis elegans* hypothetical protein ZK512.3

Query Match 4.8%; Score 294; DB 2; Length 1418;

Best Local Similarity 20.2%; Pred. No. 1.2e-12;

Matches 222; Conservative 174; Mismatches 437; Indels 264; Gaps 45;

QY 65 PNLVSVLVEGEOPFAMKSWLRDLVRKGLVKAQSGTAWILTALRVGLARHVGQAVRHS 124

Db 67 PDLIISLISHGNSLSTK--YMSSVENGLKSLFGTGLTGLISG-----EVNDPM 113


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Db 430 LELIVVMYVIGFVEEVEQEIFAVGMKS-----YLRNMWNFIDLRNSLY-VSMVC-L 479
QY 827 LPSAFEGRTVLAMD-----FMVFT-LRLIHFIAHKOL 859
Db 480 RAFAYIQOATEIARDQOMAYIPREKXHDHDPQIIAEBGLFAANVPSALKLVHLFSINPHL 539
QY 860 GKIIIVVERMMKDV--FFLFFLSVMLVAYGV--TOALLPHPHDGRLEW-- 904
Db 540 GPLQISLGRMVIDIVKFFIYTLVLFACGLNQLLWYFAALEKSKCYLVP-GGEADWGS 598
QY 905 -----IFRRV--LYRP-----YLOIFGQPLDEIDARVNCSTHPLLEDSPSCPSLYAN 952
Db 599 HGDSCMKRFRGNLFESSOSLFWASFSGMVGLODFELSGIKS-----YTR 642
QY 953 MLVILLVTLVTLVNTVLLNMLLIAMPSYTFQVQGNADMFWKFORYNLIVEHERPA-LA 1011
Db 643 FWGLLMFGSYVINVLNLLNMLIAMSNSYAMIDEHSDTEWKFPARTKYMWSYFEDSATLP 702
QY 1012 PPFILLSHLSLTLRRVFKKEAEHKREHLERDLPDLDQKVVTWETVQKENFLSKMEKRER 1071
Db 703 PPFNVLPVKWVI-RIFRKS-----KTIDRQSRKKRKEQEQF 739
QY 1072 DSEGEVLRTAHRVDIAKVLGLREQ-----EKRIKLESQIN 1110
Db 740 SEYDNIMR-----SLVMRYVAAHMKRFENNPVSEDDINEVKSEIN 779

RESULT 9
F88391
protein R06B10.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: F88391
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F88391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-899 <STO>
A:Cross-references: GB:chr_III; PIDN:AAB95033.1; PID:g2746879; GSPDB:GN00021; CBSP:R06B1
A:Gene: R06B10.4
A:Map position: 3

Query Match 4.1%; Score 247; DB 2; Length 899;
Best Local Similarity 19.4%; Pred. No. 1.6e-09;
Matches 166; Conservative 125; Mismatches 312; Indels 252; Gaps 38;

QY 349 LDELKLAANDRDVDTAKSIFNGDVWVKSCDL-----EVMVDALVNKKEPFVRLFVD 401
Db 32 LREKQFLSCERGDIGSVRKLLAGISTETFNCLDPLGRNALLIAIENIEMIELLID 91
QY 402 NGADVADFTYKGLQLYRSVSRKSLFLDLQKQF-EARLTLAGLGTQOAREPPAGPA 460
Db 92 HNIETGDAILYAIGEB---NVRAVEIIVHEKMDKPFDSERQGVETHSATPTDITPIV 148
QY 461 FSLHEVSRVLKDFLODACRGFYQDGRGDRRAEKGPAKRP-----TGQWLL 508
Db 149 LAAH-----KQYE--CIKFLD-----KKGTVPHPHDVRCSPCEYVAREEDSL 191
QY 509 DLNQKSENPRDILFWAVL-QRHEWATYFWAMQGVGAALAAACKILKEMSHLETEABA 567
Db 192 RLSRGRINAYRALTSPLSICLSARDPILYAFELSW-----LXLRSFIENEFT 240
QY 568 ARATREAKYERLALDLFSCYNSSEARAFALLVRNRCSKTTCT-----LHLAT 616
Db 241 DYEEISQKQKFCVHMDQVRGSKLE--VNLNHTTNAHVDVTSANYGNPEKLARLKLA 298
QY 617 EADAKAFFAHDGVQAFLTRIWMGDMAAGTPILRLLAGFLCPALVNTLITFSEAPLRTG 676

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Db 299 QLSQKRFVAHPNCQQLLLDIWY-----EGVESYR-----CTNFIY-KLIFY----- 338
QY 677 LEDQLDLSLDTKESPLYGLQSRVELVEAPRAQGRGPRAVFELL---TRWRKFWCAPVT 733
Db 339 -----ILGMLSPFLFSL-----VYLLAPHSMGQFAKKPFI 369
QY 734 VFLGNVMYFAFLFLFTY-----VLLVD-----FRPPQSGSGPEVTLYFWVFT 777
Db 370 KFLSHSGSYIFLILLIMASQRMNVIDNLTDDVDVKETRGPP---PTIIECAFLWVLG 427
QY 778 LVLEIRQ---GFPTDETHLVKFKTLYVGNMKNKDMVAIFLFTVGTTCRLM----- 827
Db 428 LIWVEIKQLWECGLYN-----YCRNLWNILDFITNSLYLCTTALRVVAYQVE 475
QY 828 PSAPFAGR-----TVLAMDFM---VF-TLRLIHFIAHFKQLGP-KII 864
Db 476 QEALRANSVHIARHLPRRDWAMDPTLLSECFATANIFSSILKLVHIFTVSPHLGPKIS 535
QY 865 VVE-----RMMKDV--FFELRFLSVMLVAYGVTTQALLPHPHGRLEWIFRRV- 909
Db 536 LGELEKFKWKKTLKRWVIDIVKFWVALVLFACGL-----NQLLWYASMR 585
QY 910 -----LYRPY-----LOIFGQPLDEIDEARVNC-----THPLL 940
Db 586 QNECNLYEQYKNEKSLSYKYEHKESCDKDYKSCSIYHTAETLFWALGLVDLTHRLK 645
QY 941 EDSPSCPSLYANWLVILLVTLVNTVLLNMLLIAMPSYTFQVQGNADMFWKFORYNL 1000
Db 646 ED-----HFLSEWTKTIFGSCYCCGSIIVLLNMLIAMSNSYQISDQDIEMKFARSRL 700
QY 1001 IVEYHERPA-LAPPFILG---SHLSILTLRRVFKKEAEHKREHLERDLPDLDQKVVTWET 1056
Db 701 FLEYFDDTATLPPPNIVPSPKSIYCHLYTKLONCTK-----LOQPSKQKSM---R 751
QY 1057 VQKENFLSKMEKRER 1071
Db 752 VESKNLAIRQRPKQ 766

RESULT 10
S44873
ZC21.2 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44873
R:Du, Z.; Waterston, R.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZC21.
A:Reference number: S44649
A:Accession: S44873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-823 <DUZ>
A:Cross-references: EMBL:L16685; NID:g289729; PIDN:AAA38168.1; PID:g289732
C:Genetics:
A:Introns: 47/2; 91/3; 144/1; 215/2; 344/3; 394/3; 440/3; 506/2; 566/3; 756/3
C:Superfamily: TRP3 protein
C:Keywords: transmembrane protein

Query Match 3.9%; Score 235.5; DB 2; Length 823;
Best Local Similarity 20.7%; Pred. No. 9.8e-09;
Matches 113; Conservative 92; Mismatches 190; Indels 151; Gaps 20;

QY 549 LAACKILKEMSHLETEAARAT---REAKYERLALDLFSECYNSSEARAFALLVRNR- 604
Db 260 LSAPKLSLDQLAPEEHEFEKETYQLQSECKQYSCDLLSQCRSEE--VIAILNKDGNV 317
QY 605 -----CWS---KTCILHLATEADAKAFHAGVQAFLTRIWMGDMAAGTPILRLGA-- 653
Db 318 NDDNIDVWASKLSRLKLAIKYEQKAFVSPHPCQLLTISIY----EGIPYRQSRGTWA 373
QY 654 --FLCPALVYTNLITFSEAPLRTGLELDQLDLSLDTKESPLYGL-----QSRVEELVE 705

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Db 426 LLILWIIGMIWSIKRLWYEGLED-----FLEESRNQLSFVNLSYLATFALKVVA 476
QY 829 -----SAFEAGRTVLAMDFMVFT-----LRLIHFAIHKQLGPKLIIVERMM 870
Db 477 HNKFHDFADRKWDADFHP--TLVAEGLFAFANVLSYLRFLFMFTTSSILGPIQISMGQML 534
QY 871 KDV--FFFLFSLVNLVAVGVTTQALLHPHDGRLEWIFRRVLYRYPYLOIF--GOIPLDRI 926
Db 535 QDFGKFLGNFLVLSFTIGLT-----QYDKGYTSKEQK 569
QY 927 D-----EARVNCSTHPLLEDSPSCPSLIYANWLV-----956
Db 570 DCVGIFCEQSQNDTFSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGEELQSFVGA 623
QY 957 LLLVTFLLVTVNLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVEY-HERPALAPPF- 1014
Db 624 VVGTVNVVVVILTKLLVAMLHKSFQLIANHEDEKWFARAKLWLSYFDDKCTLPFPFN 683
QY 1015 -----ILLSHLSLTLRRVFKKEAEHKEHLE--RDLDPDLQKVVTVETVQK--- 1059
Db 684 IIPSPKTCIMYMISSLSKWICSHTSKGVKVRQNSLKWRNLKQKD-----ENYQVMCC 737
QY 1060 --ENFLSKMKERRRSEGEVLRKTAHRVDFIAKYLGLRE 1097
Db 738 LVHRYLTSMRQKMQSTDOATVENELRQDLSKFRNEIRD 777
RESULT 13
I38361
TRPC1 protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
C:Accession: I38361
R:Res, P.D.; Chevessich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: I38361; MUID:96003837; PMID:7568191
A:Accession: I38361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

Query Match 2.9%; Score 176.5; DB 2; Length 810;
Best Local Similarity 18.1%; Pred. No. 0.00019;
Matches 116; Conservative 106; Mismatches 215; Indels 203; Gaps 27;
QY 555 LKEMSHLETE-----AEARATREAKYERLALDLFSECYSNSBARAF-----596
Db 261 LKELSLIVEFRNDYEELAR-----QCKMFAKDLQAQNSRLEVLNHTSSDEPLDKR 315
QY 597 ALLVRRNCWSTCTLIHLATEADAKFAFHGDGVQAFTRIRWGDMAA--GTPILRLGAF 654
Db 316 GLLEER---MNLRLKLAIKYKQEFVSQSNQQLNTWFGMSGYRRKPTCKKIMTV 371
QY 655 LCPALVYTNLITPSEEAPLTGLEDLQDLSLDTESPLYGQSVEELVEAPRAQDGRG 714
Db 372 LTVGIFW-----PVLSLCYLIT-----APKQ-----392
QY 715 PRAVELLTRKPKWGPVTVFLGNVVMYPAFLFTYVLLVDFRPPPPQSGS-----EV 769
Db 393 -----FGRIHTPFMKFIHGASYFTFLLLNLSLV-YNEDKNTMGALERIDY 442
QY 770 TLYFWVFTLVLEIROGFTFD-EDTHLVKKFTLYVGDNNKMDMAIFLFIIVGTCRMLP 828
Db 443 LLILWIIGMIWSIKRLWYEGLED-----FLEESRNQLSFVNLSYLATFALKVVA 493
QY 829 -----SAFEAGRTVLAMDFMVFT-----LRLIHFAIHKQLGPKLIIVERMM 870
Db 494 HNKFHDFADRKWDADFHP--TLVAEGLFAFANVLSYLRFLFMFTTSSILGPIQISMGQML 551

QY 871 KDV--FFFLFSLVNLVAVGVTTQALLHPHDGRLEWIFRRVLYRYPYLOIF--GOIPLDRI 926
Db 552 QDFGKFLGNFLVLSFTIGLT-----QYDKGYTSKEQK 586
QY 927 D-----EARVNCSTHPLLEDSPSCPSLIYANWLV-----956
Db 587 DCVGIFCEQSQNDTFSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGEELQSFVGA 640
QY 957 LLLVTFLLVTVNLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVEY-HERPALAPPF- 1014
Db 641 VVGTVNVVVVILTKLLVAMLHKSFQLIANHEDEKWFARAKLWLSYFDDKCTLPFPFN 700
QY 1015 -----ILLSHLSLTLRRVFKKEAEHKEHLE--RDLDPDLQKVVTVETVQK--- 1059
Db 701 IIPSPKTCIMYMISSLSKWICSHTSKGVKVRQNSLKWRNLKQKD-----ENYQVMCC 754
QY 1060 --ENFLSKMKERRRSEGEVLRKTAHRVDFIAKYLGLRE 1097
Db 755 LVHRYLTSMRQKMQSTDOATVENELRQDLSKFRNEIRD 794
RESULT 14
T34472
Hypothetical protein W03B1.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34472
R:Miller, N.; Bradshaw, H.; Wu, X.; Gattung, S.
submitted to the EMBL Data Library, June 1998
A:Description: The sequence of C. elegans cosmid W03B1.
A:Reference number: Z21532
A:Accession: T34472
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-823 <MIL>
A:Cross-references: EMBL:U58753; PIDN:AAC24437.1; GSPDB:GN00022; CESP:W03B1.2
A:Experimental source: strain Bristol N2; clone W03B1
C:Genetics:
A:Gene: CESP:W03B1.2
A:Map position: 4
A:Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2
Query Match 2.7%; Score 165; DB 2; Length 823;
Best Local Similarity 22.9%; Pred. No. 0.0014;
Matches 104; Conservative 64; Mismatches 175; Indels 112; Gaps 21;
QY 771 LYFWFTLV-----LBEIRQ---GPTDEDTHLVKKFTLYVGDNNKMDMAIFLFIIVGV 822
Db 406 LAFWRIVLVVPLLTLEAARLLIFAFVIEKKSSDKNF-----WSGA-----WVLIPI 452
QY 823 TCRMLPSAFEAGRTVLAMDFMVFTLRLIHI FAHKOLGPKLIIVERMMKDV-FFFLFPLS 881
Db 453 TLELLYCALFATAT-----VSTLRFFHSI---QSLGFFIHLFKOMKMTVGMFIIFCT 502
QY 882 VMLVAVGVTTQALLHPHDGRL-----EWIFRRVLYRYPYLOIFGOIPLDRIEAVR---N 932
Db 503 FWFVL-----AVIHVVISRTLLATSNISFLYTVTFQKFEIAGEVQ-----DEDIGILLN 552
QY 933 CSTHPLLED-----SPSCPSLIYANWLVLLVTFLLVTVNLLMNLIIAMFSYTFQV 985
Db 553 CSEYNKTMVEFFDMBYAEASC--LFRSTIMPFVFTYIFVTGILLVNLITAOULTKEYENE 610
QY 986 QGNADMFWKFORYNLIVEYHERPALAPPFIL-----1017
Db 611 SKNSAYKYLKYEQUTKIESKLYLPPPSFLVVLRFWYSCFFKIVIFTWLTSGCCK 670
QY 1018 ---SHLSLTLRRVFKKEAEHKEHLELDLPDLQKVVTVETVQKFNLSKME-----K 1068
Db 671 CSSTAISLYWRNIVRIVEGYPGAVRQTDNEIDTKVAEFLRKPDPNALEKULVNNYD 730
QY 1069 RRDSEGEVLRKTAHRV-DFIAKYLGLREQKRIKCLSQINYSVSVSSVADVLAQGG 1127
Db 731 KOVDDE-EALKKLGKIKKFLAKEIG--ERERAAQSNLENHPRSGVLDPKKKHRLS--- 784

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:01:53 ; Search time 71 Seconds
(without alignments)
5177.165 Million cell updates/sec

Title: US-10-026-188-8
Perfect score: 6093
Sequence: 1 MQDVQGPFGSGDAEDRRRE.....HRGGLDGMQPGAGPPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6093	100.0	1165	4 Q9NZQ8	Q9nzq8 homo sapien
2	6039	99.1	1159	4 Q9NY34	Q9ny34 homo sapien
3	5088.5	83.5	1158	11 Q9JUH7	Q9jyh7 mus musculus
4	5036.5	82.7	1148	11 Q9EPM4	Q9epm4 mus musculus
5	5026.5	82.5	1148	11 Q9NFM9	Q9nfm9 mus musculus
6	4981.5	81.8	1116	11 Q9EPM3	Q9epm3 mus musculus
7	4465.5	73.3	1030	11 Q8BS44	Q8bs44 mus musculus
8	4354.5	71.5	1000	11 Q7TPL4	Q7tpl4 mus musculus
9	2448.5	40.2	1214	4 Q8TD43	Q8td43 homo sapien
10	2399.5	39.4	1213	11 Q7TN37	Q7tn37 mus musculus
11	2184.5	35.9	1040	4 Q96L84	Q96l84 homo sapien
12	2164	35.5	1016	4 Q9NKV1	Q9nxv1 homo sapien
13	2098	34.4	1069	4 Q725D9	Q725d9 homo sapien
14	2069	34.0	945	11 Q8BLM7	Q8blm7 mus musculus
15	2021	33.2	1507	11 Q91YD4	Q91yd4 mus musculus
16	1722	28.3	793	11 Q80Y94	Q80y94 mus musculus

Q8r4d5 mus musculus
Q7t0w9 xenopus lae
Q8r455 rattus norv
Q72zw7 homo sapien
Q8tdx8 homo sapien
Q8tac3 homo sapien
Q86ul0 homo sapien
Q86wk3 homo sapien
Q86200 homo sapien
Q86wk2 homo sapien
Q86sh6 homo sapien
Q86wk1 homo sapien
Q86wk4 homo sapien
Q86201 homo sapien
Q86sh0 homo sapien
Q86yz9 homo sapien
Q724n1 homo sapien
Q75560 homo sapien
Q724n5 homo sapien
Q724n2 homo sapien
Q724n4 homo sapien
Q925b2 mus musculus
Q923j1 mus musculus
Q91lq1 mus musculus
Q9bxb2 homo sapien
Q96ct4 homo sapien
Q9b384 homo sapien
Q8cir4 mus musculus
Q80yb3 mus musculus

ALIGNMENTS

RESULT 1

Q9NZQ8 PRELIMINARY; PRT; 1165 AA.
AC Q9NZQ8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MTRI.
GN MTRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20076317; PubMed=10607831;
RA Prawitt D., Enklaar T., Klemm G., Gaertner B., Spangenberg C., Winterpacht A., Higgins M., Pelletier J., Zabel B.;
RT Identification and characterization of MTRI, a novel gene with homology to melastatin (MLSN1) and the trp gene family located in the BWS-WT2 critical region on chromosome 11p15.5 and showing allele-specific expression.";
RL Hum. Mol. Genet. 9:203-216(2000).
DR EMBL; AF177473; AAF26288.1; -.
DR Genew; HGNC:14323; TRPM5.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; ion_trans; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1165 AA; 131450 MW; C4AD5BAA866BE73B CRC64;

Query Match 100.0%; Score 6093; DB 4; Length 1165;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQDVQGPFGSGDAEDRRRELGLHRGEVNFVFGSGKKRKFVRVPSGVAPSLFDLLAEW 60

Db 1 MQDVQGPFGSGDAEDRRRELGLHRGEVNFVFGSGKKRKFVRVPSGVAPSLFDLLAEW 60

Qy 61 HLPAPNLVSVLVEEQPFAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
Db 61 HLPAPNLVSVLVEEQPFAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
Qy 121 RDHSLASTSTKVRVAVGMSASLGRVLRHRRILKEAQQEDPPVHYPPDDGGSGQPLCSLDSNL 180
Db 121 RDHSLASTSTKVRVAVGMSASLGRVLRHRRILKEAQQEDPPVHYPPDDGGSGQPLCSLDSNL 180
Qy 181 SHFLLVPEPPGKDGTLRLRLKXHSQAGYGGTGSIEIPIVCLLVNGDNTLRI 240
Db 181 SHFLLVPEPPGKDGTLRLRLKXHSQAGYGGTGSIEIPIVCLLVNGDNTLRI 240
Qy 241 SRVVEQAPWLLVSGGGIADVLAALVNOPHLLVPKVAEQKFKFSKHSWEDIVRW 300
Db 241 SRVVEQAPWLLVSGGGIADVLAALVNOPHLLVPKVAEQKFKFSKHSWEDIVRW 300
Qy 301 KLLQNTSHQHLTVYDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDR 360
Db 301 KLLQNTSHQHLTVYDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDR 360
Qy 361 VDIKSEIFNGDVWKSCLDEEVVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYR 420
Db 361 VDIKSEIFNGDVWKSCLDEEVVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYR 420
Qy 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
Db 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
Qy 481 FYQDGRPGDRRAEKGPAKRTGQKWLDLNOKSENPRWDLFLMAVLNQRHEMATYFWAM 540
Db 481 FYQDGRPGDRRAEKGPAKRTGQKWLDLNOKSENPRWDLFLMAVLNQRHEMATYFWAM 540
Qy 541 GOEGVAAALACKLILKENSHELEAARATREAKYERLADLDLSECVSNSEARAFALLV 600
Db 541 GOEGVAAALACKLILKENSHELEAARATREAKYERLADLDLSECVSNSEARAFALLV 600
Qy 601 RNRCSKTTCLHLATEADAKAFADHGVQAFLTRIWMGDMAGTPPIRLILGAFICPALV 660
Db 601 RNRCSKTTCLHLATEADAKAFADHGVQAFLTRIWMGDMAGTPPIRLILGAFICPALV 660
Qy 661 YTNLITFSEAPLRTGLDQLDLSLDEKSPYGLQSRVBEELVEAPRAQDGRGPRVFL 720
Db 661 YTNLITFSEAPLRTGLDQLDLSLDEKSPYGLQSRVBEELVEAPRAQDGRGPRVFL 720
Qy 721 LTRMRKFWGAPVTFLGNVMMYFAFLFTYVLLVDRPPPGSGPBEVTLVFWFTLV 780
Db 721 LTRMRKFWGAPVTFLGNVMMYFAFLFTYVLLVDRPPPGSGPBEVTLVFWFTLV 780
Qy 781 BEIRQGFTEDETHLVKKFTLVYVGNMKNKDMVAIFLFIIVGVTCTRMFLPSAFEAGRTVLAM 840
Db 781 BEIRQGFTEDETHLVKKFTLVYVGNMKNKDMVAIFLFIIVGVTCTRMFLPSAFEAGRTVLAM 840
Qy 841 DMVFTLRLIHFATHKQIGPKIIIVVERMKDVFFLFLSVLVAAGTQALLHPHDG 900
Db 841 DMVFTLRLIHFATHKQIGPKIIIVVERMKDVFFLFLSVLVAAGTQALLHPHDG 900
Qy 901 RLEWIFRVLVPEYLIQIFQIIPDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
Db 901 RLEWIFRVLVPEYLIQIFQIIPDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
Qy 961 TFLVTVNLLNLLIAMFSTYFQVQGNADMEWKFQRYNLIVVEYHERPALAPPPFILLSHL 1020
Db 961 TFLVTVNLLNLLIAMFSTYFQVQGNADMEWKFQRYNLIVVEYHERPALAPPPFILLSHL 1020
Qy 1021 SUTLRVPKKEAHEKHEHLERDLPDLDQKVTVTWETVQKNFLSKWEKERRDSEGEVLK 1080
Db 1021 SUTLRVPKKEAHEKHEHLERDLPDLDQKVTVTWETVQKNFLSKWEKERRDSEGEVLK 1080
Qy 1081 TAHRVDFTAKYLGGLREQBKRICKLESQINYCSVLVSSVADVLAQGGGPRSSQHCQEGSQ 1140
Db 1081 TAHRVDFTAKYLGGLREQBKRICKLESQINYCSVLVSSVADVLAQGGGPRSSQHCQEGSQ 1140

Qy 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165
RESULT 2
Q9NY34
ID Q9NY34 PRELIMINARY; PRT: 1159 AA.
AC Q9NY34;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LTRPCS protein (Fragment).
GN LTRPCS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Paulsen M., El-Maarri O., Engemann S., Franck O., Stroedicke M.,
RA Davies K.R., Bowden L.M., Reinhardt R., Reik W., Harteneck C.,
RA Walter J.;
RT "Comparative sequence analysis and characterization of the imprinting
RT cluster on the human chromosome 11p15.5 and distal mouse chromosome
RT 7.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ270996; CAB66342.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005281; F: cation channel activity; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ionic channel; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 1159 AA; 130775 MW; E3165B8C1125363B CRC64;
Query Match 99.1%; Score 6039; DB 4; Length 1159;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1157; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Qy 9 PGSGDADRDRELGLHGRGEVNFSGSKRGKRGKRVFVPSVAPSVLFDLLAEHLAPNLV 68
Db 1 PGSGDADRDRELGLHGRGEVNFSGSKRGKRGKRVFVPSVAPSVLFDLLAEHLAPNLV 60
Qy 69 VSLVGEOPPFAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGQAVRDHSLAST 128
Db 61 VSLVGEOPPFAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGQAVRDHSLAST 120
Qy 129 STKVRVAVGMSASLGRVLRHRRILKEAQQEDPPVHYPPDDGGSGQPLCSLDSNL 186
Db 121 STKVRVAVGMSASLGRVLRHRRILKEAQQEDPPVHYPPDDGGSGQPLCSLDSNL 180
Qy 187 EPGPPKDGTLRLRLKXHSQAGYGGTGSIEIPIVCLLVNGDNTLRI 246
Db 181 EPGPPKDGTLRLRLKXHSQAGYGGTGSIEIPIVCLLVNGDNTLRI 240
Qy 247 AAPWLLVSGGGIADVLAALVNOPHLLVPKVAEQKFKFSKHSWEDIVRWTKLLQNI 306
Db 241 AAPWLLVSGGGIADVLAALVNOPHLLVPKVAEQKFKFSKHSWEDIVRWTKLLQNI 300
Qy 307 TSHQHLTVYDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDRVDIAKS 366
Db 301 TSHQHLTVYDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDRVDIAKS 360
Qy 367 EIFNGDVWKSCLDEEVVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYR 426
Db 361 EIFNGDVWKSCLDEEVVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYR 420
Qy 427 LIFDQLQKQBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRGFYQDGR 486
Db 421 LIFDQLQKQBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRGFYQDGR 480

QY 487 PGDRRAEKGPAPKPTCKQKLLDINOKSENPRDLFLWAVLQNRHEMATYFWAMQSGVA 546
 DB 481 PGDRRAEKGPAPKPTCKQKLLDINOKSENPRDLFLWAVLQNRHEMATYFWAMQSGVA 540
 QY 547 AALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSEARAFALLVRRNCW 606
 DB 541 AALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSEARAFALLVRRNCW 600
 QY 607 SKTTCLHLATEADAKAFHAGDGVQAFLTRIWWGDMAGTPTLRLGAFGLCPALVYTNLIT 666
 DB 601 SKTTCLHLATEADAKAFHAGDGVQAFLTRIWWGDMAGTPTLRLGAFGLCPALVYTNLIT 660
 QY 667 FSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRPRAVFLTLTWRK 726
 DB 661 FSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRPRAVFLTLTWRK 720
 QY 727 FWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQSPGPEVTLFWVFTLVLEIRQG 786
 DB 721 FWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQSPGPEVTLFWVFTLVLEIRQG 780
 QY 787 FFTDETHLVKFTLVGNWNKCDMVAIFLFIYGVTCRMLPSAFAGRTVLAMDWFVFT 846
 DB 781 FFTDETHLVKFTLVGNWNKCDMVAIFLFIYGVTCRMLPSAFAGRTVLAMDWFVFT 840
 QY 847 LRLIHFAIKHQLGPKIIVVERMMKDVFFLFLSVLVAIVYVTTQALLHPHGRLEWIF 906
 DB 841 LRLIHFAIKHQLGPKIIVVERMMKDVFFLFLSVLVAIVYVTTQALLHPHGRLEWIF 900
 QY 907 RRVLYRPYLQIQOIPDLDEIDARVNCSTHPLLESPPCSYIYANWLVILLVTFLLVT 966
 DB 901 RRVLYRPYLQIQOIPDLDEIDARVNCSTHPLLESPPCSYIYANWLVILLVTFLLVT 960
 QY 967 NVLLNMLLIAMFSYTFQVVGQNMDFWKFORYNLIVEYHERPALAPPEFILLSHLSLTLRR 1026
 DB 961 NVLLNMLLIAMFSYTFQVVGQNMDFWKFORYNLIVEYHERPALAPPEFILLSHLSLTLRR 1020
 QY 1027 VPKKEAEHREHLERDLDPDQKVVTWETVQKENFLSKMEKRRRDESEGLRKTARVD 1086
 DB 1021 VPKKEAEHREHLERDLDPDQKVVTWETVQKENFLSKMEKRRRDESEGLRKTARVD 1080
 QY 1087 FTAKYLGGLREOEKRIKCLSEQINYSVLVSSVADYLAQGGPRSSQHGEGSOLVAADH 1146
 DB 1081 FTAKYLGGLREOEKRIKCLSEQINYSVLVSSVADYLAQGGPRSSQHGEGSOLVAADH 1140
 QY 1147 RGLDGEQPGAGQPPSDT 1165
 DB 1141 RGLDGEQPGAGQPPSDT 1159

RESULT 3
 Q9JUH7
 ID Q9JUH7 PRELIMINARY; PRT; 1158 AA.
 AC Q9JUH7;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE MLSN1-and TRP-related protein 1 (MTR1) (Transient receptor potential
 DE cation channel subfamily M member 5).
 GN TRPM5 OR LTRPM5 OR MTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP PubMed=10907850;
 RA Yatsuki H., Watanabe H., Hattori M., Joh K., Soejima H., Komoda H.,
 RA Xin Z., Zhu X., Higashimoto K., Nishimura M., Kuratomi S., Sakaki H.,
 RA Sakaki Y., Mukai T.;
 RT "Sequence-based structural features between Kv1qt1 and Tapal on mouse
 RT chromosome 7F4/F5 corresponding to the Beckwith-Wiedemann syndrome
 RT region on human 11p15.5: long-stretches of unusually well conserved

intronic sequences of Kv1qt1 between mouse and human.";
 DNA Res. 7:195-206(2000).

[2]

SEQUENCE FROM N.A.

MEDLINE=20366135; PubMed=10903843;

Enklaar T., Esswein M., Oswald M., Hilbert K., Winterpacht A.,

Higgins M., Zabel B., Prawitt D.;

"Mtr1, a Novel Biallelically Expressed Gene in the Center of the Mouse

Distal Chromosome 7 Imprinting Cluster, is a Member of the Trp Gene

Family.";

Genomics 67:179-187(2000).

[3]

SEQUENCE FROM N.A.

STRAIN=129/SvxC57BL; TISSUE=lung;

MEDLINE=22726392; PubMed=12842017;

Hofmann T., Chubakov V., Gudermann T., Montell C.;

"TRPM5 is a Voltage-Modulated and Ca(2+)-Activated Monovalent

Selective Cation Channel.";

Curr. Biol. 13:1153-1158(2003).

EMBL; AB039952; BAA96877.1; -

EMBL; AF228681; AAF98120.1; -

EMBL; AY280364; AAF44476.1; -

MED; MGI:1861718; Trpm5.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005261; F:cation channel activity; IEA.

GO; GO:0006812; P:cation transport; IEA.

InterPro; IPR002111; Cat_channel_trpL.

InterPro; IPR005821; Ion_trans.

Pfam; PF00520; ion trans; 1.

KW Ionic channel; Receptor; Transmembrane.

SEQUENCE 1158 AA; 130843 MW; FOA5237EC67867CE CRC64;

Query Match

Best Local Similarity 83.5%; Score 5088.5; DB 11; Length 1158;

Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MDQVQPRPGSGDADREELGLHGEVNFVFGSGKKRGKRVFVPSVAPSVLFLLLAEW 60

DB 1 MOTTQSSCGSPDTEDEWEPILCGRINFGSGKKRGKRVFVPSVAPSVLFLLLTEW 60

QY 61 HLPAPNLVSVLVEGEQPFAMKSWLRDLVRKGLVKAAQSTGAMILTSALRVGLARHVQAV 120

DB 61 HLPAPNLVSVLVEGEERPLAMKSWLRDLVRKGLVKAAQSTGAMILTSALRVGLARHVQAV 120

QY 121 RDHSLASTTKRVVAVGVASLGRVLRRLILE--EAQEDFPVHYDEDDGGSGQPLCSLDS 178

DB 121 RDHSLASTTKIRVVAIGNASLDRLHRLQLLDGVHQKEDTRIHYFADEGNIQGFPLCLDS 180

QY 179 NLSHFILVPEPGPGKG-DGLTELRLRLKLEHISEQAGYGGTSGIETPVLCLLVNGDPNTL 237

DB 181 NLSHFILVPEGALGSGNDGLTELQSLKHIISQRTGYGTSCIQIPVCLLVNGDPNTL 240

QY 238 ERISRAVEQAAPWLILVSGGGIADVLAALVNQPHLLVPKVAEKQFKEPPSKHFSWEDIV 297

DB 241 ERISRAVEQAAPWLILVSGGGIADVLAALVSPHLLVPQVAEKQFKEPPSCFSEALV 300

QY 298 RTWKLQNTSHOHLITVYDFEQQSELDVILKALVKACKSHQSQEQDYDELKLA 357

DB 301 HNTLQNTIAHPHLLTYVDFEQSELDVILKALVKACKSHQSQEQDYDELKLA 360

QY 358 WDRVDIAKSEIFNGDVWKSQDLEBVMYDALVSNKPEFVFLVDNGADVADFLTYGRLOE 417

DB 361 WDRVDIAKSEIFNGDVWKSQDLEBVMYDALVSNKPEFVFLVDNGADVADFLTYGRLOE 420

QY 418 LYRSVSRKSLFDLQKQEEARLTLAGLGTQAREPPAGPPAFSLHVSRLVDFLODA 477

DB 421 LYHSVSPKSLFDLQKQEEARLTLAGLGTQAREPPAGPPAFSLHVSRLVDFLODA 480

QY 478 CRGFYQDGRDRAAEKGPAPKPTGQKWLDDLNOKSENPRDLFLWAVLQNRHEMATYF 537

DB 481 CRGFYQDGRDRAAEKGPAPKPTGQKWLDDLNOKSENPRDLFLWAVLQNRHEMATYF 536

QY 538 WAMQGEVAAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSEARAF 597

Db 537 WAMGREGVAAALAAACKIIKEMSHLEKEAEVARTWREAKYEQALDLDFSECYGNSEDRAFA 596
Qy 598 LLVRNRCWKTTCCLHLATEADAKAFHAGDVGQAFLTRIWMGDMAGTPTILRLGAFCLP 657
Db 597 LLVRNHSWSRTTCLHLATEADAKAFHAGDVGQAFLTRIWMGDMATGPTILRLGAFCTP 656
Qy 658 ALVVTNLITFSEAPLRTGLELDLDLSDTEKSPLYGLQSRVBEVLEAPRAQDGRGPA 717
Db 657 ALIYTNLISFSEDAPQRMDELDLQEPDSLDMEKSFCLSRGQLEKLTAPAPGDLGPOA 716
Qy 718 VELLTRWRKFWGAPVTVFLGNVVMYFAFLFTVTVLLVDPRPPQSGSGPBVTLYFWVFT 777
Db 717 AFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTVTVLLVDPRPPQSGSGPBVTLYFWVFT 776
Qy 778 LVLEETIRQGFDTDETHLVKFTLYVGNWNKCDMVAIFLIVGVTCTMLPSAFEAGRTV 837
Db 777 LVLEETIRQGFDTDETHLVKFTLYVGNWNKCDMVAIFLIVGVTCTMLPSAFEAGRTV 836
Qy 838 LAMDFWFTLRLIHI FAHKQLGPKIIIVVERMKDVFPEFFFLSVLWVAYGVTTQALLHP 897
Db 837 LAIDFWFTLRLIHI FAHKQLGPKIIIVVERMKDVFPEFFFLSVLWVAYGVTTQALLHP 896
Qy 898 HDGRLEWIFRRVLYRPLYQIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 957
Db 897 HDGRLEWIFRRVLYRPLYQIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 956
Qy 958 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFQKRYNLIIVYHERPALAPFFILL 1017
Db 957 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFQKRYNLIIVYHERPALAPFFILL 1016
Qy 1018 SHLSITLRRVFKAEHREHLERDLPDQKVVTWETVQENFLSKMERKRRDSEGV 1077
Db 1017 SHLSVLKQVRKEAQHRLERDLPDQKVVTWETVQENFLSKMERKRRDSEGV 1076
Qy 1078 LRKTAHRVDFIAKYLGRLREOKRIKLESQINYSVLSVADVIAOGGPRSSOHCE 1137
Db 1077 LRKTAHRVDFIAKYLGRLREOKRIKLESQINYSVLSVADVIAOGGPRSSOHCE 1136
Qy 1138 GSQVLAADHRGGLDQWEGQAGQPPSDT 1165
Db 1137 RSQASARDREYLE-----SGLPSPSDT 1158

RESULT 4
Q9EPM4
ID Q9EPM4 PRELIMINARY; PRT; 1148 AA.
AC Q9EPM4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE LTRC5 protein.
GN TRPM5 OR LTRPC5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX MEDLINE=20377495; PubMed=10915772;
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841(2000).
DR EMBL; AJ251835; CAC19456.1; -.
DR MGD; MGI:1861718; Trpm5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.

DR Pfam; PF00520; ion_trans; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1148 AA; 129630 MW; 947AF5B9CFDCA127 CRC64;

Query Match 82.7%; Score 5036.5; DB 11; Length 1148;
Best Local Similarity 85.5%; Pred. No. 0;
Matches 966; Conservative 63; Mismatches 94; Indels 7; Gaps 3;

Qy 1 MQDVQSGPRPGSGDAEDRRELGLHRGEVNFPGSGKKGKGVFVPSGVAPSVFLPILLAEW 60
Db 1 MQTTSQSCPGSPDPTDGEWPILCRGEINFGSGKKGKGVFVPSGVAPSVFLPILLAEW 60
Qy 61 HLPAPNLVSLVGEQPFAMKSWLRDLRWGLVKAAGSTGAWILTSALRVGLARHVGQAV 120
Db 61 HLPAPNLVSLVGEQPFAMKSWLRDLRWGLVKAAGSTGAWILTSALRVGLARHVGQAV 120
Qy 121 RDHSLASTSTKRVVAVGMASLGRVLRHRLILE--EAQEDFPVHYPEDDGGSGQSLCLSDS 178
Db 121 RDHSLASTSTKRVVAVGMASLGRVLRHRLILE--EAQEDFPVHYPEDDGGSGQSLCLSDS 180
Qy 179 NLSHFILVERPGPGKG-DGLTELRLEKHSRAGYGGTGSIEIPVLCLLVNGDPTL 237
Db 181 NLSHFILVERPGPGKG-DGLTELRLEKHSRAGYGGTGSIEIPVLCLLVNGDPTL 240
Qy 238 ERISRAVEQAPWLLIYSGGIAADVLAALYNOPHLVPAEAKOFKEKFPKSHFSWEDIV 297
Db 241 ERISRAVEQAPWLLIYSGGIAADVLAALYNOPHLVPAEAKOFKEKFPKSHFSWEDIV 300
Qy 298 RWTKLQNTSHOHLITVYDFEQSGSELDVTILKALVKACKSHSQEPQDYLDELKLA 357
Db 301 HWTLLQNTSHOHLITVYDFEQSGSELDVTILKALVKACKSHSQEPQDYLDELKLA 360
Qy 358 WDRVDIAKSEITFNGDVEWKSQDLBEVMDALVSNKPEFVRLFVNGADVAADFLTVGRLOE 417
Db 361 WDRVDIAKSEITFNGDVEWKSQDLBEVMDALVSNKPEFVRLFVNGADVAADFLTVGRLOE 420
Qy 418 LYRSVRSKSLFDLLQKQEEARLTLAGLGTQQAAREPPAGPAPFSLHVSRLVKDLQDA 477
Db 421 LYHSVSPKSLFELLQKHEEGRLLTAGLGAQAARELPIGLAPFSLHVSRLVKDLQDA 480
Qy 478 CRGFYQDGRPGDRRAEKGPAKRPTGQKWLDDLMQKSENPRDILFWALVQNRHMAATYF 537
Db 481 CRGFYQDGRPGDRRAEKGPAKRPTGQKWLDDLMQKSENPRDILFWALVQNRHMAATYF 536
Qy 538 WAMQGVAAALAAACKIILKEMSHLETEABARAAREAKYERLADLFSECIYNSBARAPA 597
Db 537 WAMQGVAAALAAACKIILKEMSHLETEABARAAREAKYERLADLFSECIYNSBARAPA 596
Qy 598 LLVRNRCWKTTCCLHLATEADAKAFHAGDVGQAFLTRIWMGDMAGTPTILRLGAFCLP 657
Db 597 LLVRNHSWSRTTCLHLATEADAKAFHAGDVGQAFLTRIWMGDMATGPTILRLGAFCTP 656
Qy 658 ALVVTNLITFSEAPLRTGLELDLDLSDTEKSPLYGLQSRVBEVLEAPRAQDGRGPA 717
Db 657 ALIYTNLISFSEDAPQRMDELDLQEPDSLDMEKSFCLSRGQLEKLTAPAPGDLGPOA 716
Qy 718 VELLTRWRKFWGAPVTVFLGNVVMYFAFLFTVTVLLVDPRPPQSGSGPBVTLYFWVFT 777
Db 717 AFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTVTVLLVDPRPPQSGSGPBVTLYFWVFT 776
Qy 778 LVLEETIRQGFDTDETHLVKFTLYVGNWNKCDMVAIFLIVGVTCTMLPSAFEAGRTV 837
Db 777 LVLEETIRQGFDTDETHLVKFTLYVGNWNKCDMVAIFLIVGVTCTMLPSAFEAGRTV 836
Qy 838 LAMDFWFTLRLIHI FAHKQLGPKIIIVVERMKDVFPEFFFLSVLWVAYGVTTQALLHP 897
Db 837 LAIDFWFTLRLIHI FAHKQLGPKIIIVVERMKDVFPEFFFLSVLWVAYGVTTQALLHP 896
Qy 898 HDGRLEWIFRRVLYRPLYQIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 957
Db 897 HDGRLEWIFRRVLYRPLYQIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 956
Qy 958 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFQKRYNLIIVYHERPALAPFFILL 1017
Db 957 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFQKRYNLIIVYHERPALAPFFILL 1016

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Db      957  LVTFLVTLNLLMLLIAMFSTFQVVGQADMFVKFQRYHLIVYHGRPALAPPFILL 1016
QY      1018  SHLSLTLRRVFKKEAEHKEHLEBRDLPDLPDQKVVTWVQKENFLSKMEKRERDSEGEV 1077
Db      1017  SHLSVLKQVFRKEAQRHLEBRDLPDLPDQKVVTWVQKENFLSKMEKRERDSEGEV 1076
QY      1078  LRKTAHRVDFAKYGLGLREQEKRICKLESQINVCYSLVSSVADVLAQGG 1127
Db      1077  LRKTAHRVDLIAKYIGGLREQEKRICKLESQANVCYMLLSMTDTLAPGG 1126

RESULT 5
Q99NF9  PRELIMINARY; PRT; 1148 AA.
AC Q99NF9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Ltrpc5 protein.
GN TRPM5 OR LTRPC5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RA Stroedicke M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RA Engemann S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271092; CAB94717.2; -.
DR MGD; MGI:1861718; Trpm5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; F:cation transport; IEA.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; ion trans. 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1148 AA; 129590 MW; 90517E8557DCA127 CRC64;

Query Match 82.5%; Score 5026.5; DB 11; Length 1148;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 965; Conservative 63; Mismatches 95; Indels 7; Gaps 3;

QY      1 MODVQGPFGSDAEDRELGLHGEVNFVGGSKRGKRVFVPSGVAPSVLFDLLLAEW 60
Db      1 MDTTSSCGSPDPTEDGNEPTLCRGEINFGGSKRGKRVFVPSGVAPSVLFDLLLAEW 60
QY      61  HLPAPNLVSVLGEERQPFAMKSWLRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db      61  HLPAPNLVSVLGEERPLAMKSWLRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
QY      121  RDHSLASTSTKRVVAVGMSLGRVHLRRILF--EAQEDFPVHYPEDDGGSGPLCLSDS 178
Db      121  RDHSLASTSTKRVVAIGMSLDRILHRLQLLDGVHQKEDTPHYPADEGNIGPLCPILDS 180
QY      179  NLSHFILVPEGPGKG-DGLTBLRLRLKHLSEQAGYGGTGSIPVLCLLVNGDPNTL 237

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Db      181  NLSHFILVESGALSGNDGLTELQLSLEKHSOORTGYGTSCTCIQIPVLCLLVNGDPNTL 240
QY      238  ERISRAVEQAAPWLLIVGSGGTADVLAAALVNPHLLVPKVAEKQFKEKPPSKHFSWEDIV 297
Db      241  ERISRAVEQAAPWLLIVGSGGTADVLAAALVQPHLLVPKVAEKQFKEKPPSKHFSWEDIV 300
QY      298  RWTKLQNTITSHOHLITVYDFEQEGSEELDTVILKALVKACKSHSOBODYDLDELKLA 357
Db      301  HWTCLQNTITSHOHLITVYDFEQEGSEELDTVILKALVKACKSHSOBODYDLDELKLA 360
QY      358  WDRVDIAKSEIFNGDVWVKSCDLEEVMDALVSNKPEFVRLFLVDNGADVADFLTYGRLOE 417
Db      361  WDRVDIAKSEIFNGDVWVKSCDLEEVMDALVSNKPEFVRLFLVDNGADVADFLTYGRLOE 420
QY      418  LYRSVSRKSLLEFLLQKQKQEARLITLGLTQOAREPPAGPAPAFSLHESRVLKDFLODA 477
Db      421  LYHSVSPKSLLEFLLQKQKQEARLITLGLTQOAREPPAGPAPAFSLHESRVLKDFLODA 480
QY      478  CRGFYQDGRPGDGRRAEKGPAPKPTGQKWLDDLNOKSENPRDLFLWAVLQNRHEMATVF 537
Db      481  CRGFYQDGRPGDGRRAEKGPAPKPTGQKWLDDLNOKSENPRDLFLWAVLQNRHEMATVF 536
QY      538  WAMQOGEVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAF 597
Db      537  WAMQOGEVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAF 596
QY      598  LLVRRNRCKSKTCLHLATEADAKAFFAHGQVQAFELTRVWGDMAAGTILRLGLFCP 657
Db      597  LLVRRNRCKSKTCLHLATEADAKAFFAHGQVQAFELTRVWGDMAAGTILRLGLFCP 656
QY      658  ALVYTNLTITFSEAPLRTGLEDLQDLSDLEKSPLYGLQSRVVEIAPRAQGDGRPA 717
Db      657  ALVYTNLTITFSEAPLRTGLEDLQDLSDLEKSPLYGLQSRVVEIAPRAQGDGRPA 716
QY      718  VLLTRWRKFWGAPVTVFLGNVVMYPAFLFTYVLLVDRPDPGQSGPEVTLYFWVFT 777
Db      717  APELLTRWRKFWGAPVTVFLGNVVMYPAFLFTYVLLVDRPDPGQSGPEVTLYFWVFT 776
QY      778  LVLESIROGFFDDETHLVKKEFLYVGDNNWKNCDMVAIFLFTVGVTCRMLPSAFAGRTV 837
Db      777  LVLESIROGFFDDETHLVKKEFLYVGDNNWKNCDMVAIFLFTVGVTCRMLPSAFAGRTV 836
QY      838  LAMDFWVFTLRILHIFAIHKQLGPKIIIVVERMKDVFVFFFLFSLVNLVAYGVTTOALLHP 897
Db      837  LAMDFWVFTLRILHIFAIHKQLGPKIIIVVERMKDVFVFFFLFSLVNLVAYGVTTOALLHP 896
QY      898  HDGRLEWIFRRVLYRPLQIFQIPLDEIDARVNCSTHPLLEDSPSPCLSYANLVL 957
Db      897  HDGRLEWIFRRVLYRPLQIFQIPLDEIDARVNCSTHPLLEDSPSPCLSYANLVL 956
QY      958  LLVTELLVTVNLLMLLITAMFSYTFQVVGQADMFVKFQRYHLIVYHGRPALAPPFILL 1017
Db      957  LLVTELLVTVNLLMLLITAMFSYTFQVVGQADMFVKFQRYHLIVYHGRPALAPPFILL 1016
QY      1018  SHLSLTLRRVFKKEAEHKEHLEBRDLPDLPDQKVVTWVQKENFLSKMEKRERDSEGEV 1077
Db      1017  SHLSLTLRRVFKKEAEHKEHLEBRDLPDLPDQKVVTWVQKENFLSKMEKRERDSEGEV 1076
QY      1078  LRKTAHRVDFAKYIGGLREQEKRICKLESQINVCYSLVSSVADVLAQGG 1127
Db      1077  LRKTAHRVDLIAKYIGGLREQEKRICKLESQANVCYMLLSMTDTLAPGG 1126

RESULT 6
Q9EPM3  PRELIMINARY; PRT; 1116 AA.
AC Q9EPM3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Ltrpc5 protein.
GN TRPM5 OR LTRPC5.
OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RX MEDLINE=20377495; PubMed=10915772;
 RA Paulsen M., El-Naari O., Engemann S., Stroedicke M., Franck O.,
 Davies K., Reinhardt R., Reik W., Walter J.;
 RA "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RL Hum. Mol. Genet. 9:1829-1841(2000).
 DR EMBL; AJ251835; CAC19457.1; -.
 DR MGD; MGI:1861718; Trpm5.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans; 1.
 DR KW Ionic channel; Transmembrane.
 SQ SEQUENCE 1116 AA; 126608 MW; 32DFFABCF2835E48 CRC64;
 Query Match 81.8%; Score 4981.5; DB 11; Length 1116;
 Best Local Similarity 85.8%; Pred. No. 0;
 Matches 956; Conservative 60; Mismatches 91; Indels 7; Gaps 3;
 QY 1 MQDVQPRPGSGDAEDRRLGLHGEVNFSGSKKRGKRVVPVSGVAPSVLFDLLAEW 60
 DB 1 MQTTQSSCPGPPPTDGEWEPILCRGEINFGSGKKRGKRVVPSSVAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSVLVEEQQPAMKSLRDLVRLKGLVKAQAQSTGAWILTSALRVGLARHVGQAV 120
 DB 61 HLPAPNLVSVLVEEQQPAMKSLRDLVRLKGLVKAQAQSTGAWILTSALRVGLARHVGQAV 120
 QY 121 RDHSLATSTKRVVAVGMSASLGRVLRHRIE--EAQEDFPVHPEDDGGSGQPLCSLDS 178
 DB 121 RDHSLATSTKRVVAVGMSASLGRVLRHRIE--EAQEDFPVHPEDDGGSGQPLCSLDS 178
 QY 179 NLSHFILVPEPPGKG-DGLTELRLRLKHHISEQAGVGGTGTETIPVLCILVNGDPNLT 237
 DB 181 NLSHFILVESGALSGNDGLTELQSLKHHISQOQTGYGGTSCQIPVLCILVNGDPNLT 240
 QY 238 ERISRAVEQAAPWILVGGSGIADVAALVNPQHLVPKVAEKQKFKFPKSHSWEDIV 297
 DB 241 ERISRAVEQAAPWILVGGSGIADVAALVNPQHLVPKVAEKQKFKFPKSHSWEDIV 300
 QY 298 RWTLLQNTSHOHLITVYDFEQSGSELDITVILKALVKAACKSHSQEPQDYLDELKLA 357
 DB 301 HWTELLQNTSHOHLITVYDFEQSGSELDITVILKALVKAACKSHSQEPQDYLDELKLA 360
 QY 358 WDRVDIAKSEIFNGDVWKSQDLERVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417
 DB 361 WDRVDIAKSEIFNGDVWKSQDLERVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 420
 QY 418 LYRSVRSKLLFDLQKQOEARTLAGLGTQQAEEPPAGPPAFSLHEVSRVLKDFLODA 477
 DB 421 LYHSVSPKLLFELLQKHEGRLLTAGLGAQAARELPGLPAFSLHEVSRVLKDFLODA 480
 QY 478 CRGFVQDGRDGRRAEAKGPAKPTGQKWLIDLNOKSENPRDILFLWVLQNRHEMATYF 537
 DB 481 CRGFYQDQ----RRMEERGPKPAGQKWLPLSRKSEDPWRDLFLWVLQNRHEMATYF 536
 QY 538 WAMQGVAAALAAACKILKMSHLTEAARATREAKYERLALDLFSECVSNSEARAF 597
 DB 537 WAMQGVAAALAAACKILKMSHLTEAARATREAKYERLALDLFSECVSNSEARAF 596
 QY 598 LLVRRNRCWSKTTCLHATEADAKAFFAGHDGVOAFLTRIWGDMAAGTPIRLLLGAFLCP 657
 DB 597 LLVRRNHSWRTTCLHATEADAKAFFAGHDGVOAFLTRIWGDMAAGTPIRLLLGAFTCP 656
 QY 658 ALVYNTLITFSEAPITRGLELDQLDLSLDTKSPLYGLOSVEELVEAPRAQGRGPA 717
 DB 717 ALVYNTLITFSEAPITRGLELDQLDLSLDTKSPLYGLOSVEELVEAPRAQGRGPA 717

DB 657 ALIYTNLISFSDAPQRMDELDQEPDSLDMKSFCLSRGQLEKLTAPAPGDLGPQA 716
 QY 718 VFLTLTRWRKFWGAPVTVFLGNVVMYFAFLFTVTVLLVDRPPPPQPGSGPEVTLYFWVFT 777
 DB 717 AFLTLTRWRKFWGAPVTVFLGNVVMYFAFLFTVTVLLVDRPPPPQPGSGSEVTLYFWVFT 776
 QY 778 LVLEERIQGFTTDETHLVKKFTLYVGDNNKCDMVAIFLTVGVTCTRMPLPSAEAGRTV 837
 DB 777 LVLEERIQGFTTDETHLVKKFTLYVGDNNKCDMVAIFLTVGVTCTRMPLPSAEAGRTV 836
 QY 838 LAMDFWVFTLRLTHIFAIHKOLGPKIIVVERMMKDVFFELFSLVWLVAVGTTQALLHP 897
 DB 837 LAIDFWVFTLRLTHIFAIHKOLGPKIIVVERMMKDVFFELFSLVWLVAVGTTQALLHP 896
 QY 898 HDGRLWIFRRVLYRYPYLIQIFGQIPLDIDEARVNCSTHPLLLSDSPCSLYANWLVL 957
 DB 897 HDGRLWIFRRVLYRYPYLIQIFGQIPLDIDEARVNCSTHPLLLSDSPCSLYANWLVL 956
 QY 958 LLVTFLLVTVNVLNMLLIAMFSYTFVQVGNADMFQKFORNLIVEHERALAPPFTLL 1017
 DB 957 LLVTFLLVTVNVLNMLLIAMFSYTFVQVGNADMFQKFORNLIVEHERALAPPFTLL 1016
 QY 1018 SHLSLTLRRVYFKKEAEHREHLERDLDPDLDQKVTVTWETVQENFLSKMKRRRDSGEV 1077
 DB 1017 SHLSLTLRRVYFKKEAEHREHLERDLDPDLDQKVTVTWETVQENFLSKMKRRRDSGEV 1076
 QY 1078 LRKTAHRVDLTAJYIGGLREQEKIKLESQINY 1111
 DB 1077 LRKTAHRVDLTAJYIGGLREQEKIKLESQSKY 1110
 RESULT 7
 Q8BS44 PRELIMINARY; PRT; 1030 AA.
 ID Q8BS44
 AC Q8BS44;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Transient receptor potential cation channel (Fragment).
 GN TRPM5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK035197; BAC28976.1; -.
 DR MGD; MGI:1861718; Trpm5.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans; 1.
 DR NON_TER 1
 SQ SEQUENCE 1030 AA; 116983 MW; DDB31B7DF238F402 CRC64;
 Query Match 73.3%; Score 4465.5; DB 11; Length 1030;
 Best Local Similarity 84.4%; Pred. No. 0;
 Matches 858; Conservative 56; Mismatches 91; Indels 11; Gaps 3;
 QY 151 LEEAQEDFPVHPEDDGGSGQPLCSLDSNLSHFLVPEPPGKG-DGLTELRLKHHIS 209
 DB 25 LSLAQEDFPVHPEDDGGSGQPLCSLDSNLSHFLVPEPPGKG-DGLTELRLKHHIS 84
 QY 210 EORAGYGGTGTETIPVLCILVNGDPNLTETLERSRAVEQAAPWILVGGSGIADVAALVNPQ 269

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Db      85  QRTGTYGGTSCIPVLCVLLVNGDPNLTIRISRAVEQAAPWLLIAGSGGIADVLAAVLSQ 144
QY      270  PHLLVPKVAEKQKPEKPSKHFQSWEDIVRMTKLLQNTTSHOHLITVYDFEQQSEELDTV 329
Db      145  PHLLVPKVAEKQKPEKPSKHFQSWEDIVRMTKLLQNTTSHOHLITVYDFEQQSEELDTV 204
QY      330  ILKALVKACKSHSQEPQDYDELKLA VAVRDVIAKSEIFNGDVEMKSCDLEEVMDALV 389
Db      205  ILKALVKACKSHSQEQADCLDELKLA VAVRDVIAKSEIFNGDVEMKSCDLEEVMDALV 264
QY      390  SNKPEFVRLVDNGADVADFLTYGRLOELYRVSRSKSLLEDILQRKQBEARLTLAGLGTQ 449
Db      265  SNKPEFVRLVDNGADVADFLTYGRLOELYRVSRSKSLLEDILQRKQBEARLTLAGLGTQ 324
QY      450  QAREPPAGPPAFSLHVSRLVLDKPDODACHGFYQDGRPGDRRAEKGPAKRPYTGOKWLLD 509
Db      325  QARELPGLGPAFSLHVSRLVLDKPDODACHGFYQDGRPGDRRAEKGPAKRPYTGOKWLLD 380
QY      510  LNKSENPMRDLFLWAVLQNRHEMATYFWAMGQGVAAALAAACKILKEMSHLETEAEAR 569
Db      381  LSRKSDPMRDLFLWAVLQNRHEMATYFWAMGQGVAAALAAACKILKEMSHLENEAEAR 440
QY      570  ATREAEYERLALDIFSECYNSSEARAPALLVRRNRCWSKTTCLHLATEADAKAFFAHGV 629
Db      441  TMEAEYEQALDLFSECYNSSEARAPALLVRRNRCWSKTTCLHLATEADAKAFFAHGV 500
QY      630  QAFLETRIMWGDMAAGTPIRLKLGAFCLPALVYNLTTFSEAEPLRGLDLODLSLDT 689
Db      501  QAFLETRIMWGDMAAGTPIRLKLGAFCLPALVYNLTTFSEAEPLRGLDLODLSLDT 560
QY      690  KSPLYGLQSRVELVEAPRAQGRGPRVFLTRMRKFWGAPVTVFLGNVVMYFAFLFLF 749
Db      561  KSPFLSRGQLEKLEAPRAPAGDLGQAAFLTRMRKFWGAPVTVFLGNVVMYFAFLFLF 620
QY      750  TVVLLVDRPPQPGSGPEVTLFWFTLVLEIRQGFDTEDTHLVKFTLYVGNWNK 809
Db      621  TVVLLVDRPPQPGSGPEVTLFWFTLVLEIRQGFDTEDTHLVKFTLYVGNWNK 680
QY      810  CDMAIFIFIVGTCTMLPSAEPAGRTVLAMDFMFTLRIHFAHKOLGPKLIIVERM 869
Db      681  CDMAIFIFIVGTCTMLPSAEPAGRTVLAMDFMFTLRIHFAHKOLGPKLIIVERM 740
QY      870  MKDVFFFLFLSVLVAYGTTQALLPHDGRLEWIFRVLRYRPLQIFQGLPDEIDA 929
Db      741  MKDVFFFLFLSVLVAYGTTQALLPHDGRLEWIFRVLRYRPLQIFQGLPDEIDA 800
QY      930  RVNCSLHPLLEDSPSCPSLYANWLVLLVTLVTLVTLVTLVTLVTLVTLVTLVTLV 989
Db      801  RVNCSLHPLLEDSPSCPSLYANWLVLLVTLVTLVTLVTLVTLVTLVTLVTLVTLV 860
QY      990  DMFWKFORVNLVYEHRRPALAPPFTLLSHLSLTLRRVFKKEAHEKHEHLERDLPDQ 1049
Db      861  DMFWKFORVNLVYEHRRPALAPPFTLLSHLSLTLRRVFKKEAHEKHEHLERDLPDQ 920
QY      1050  KVVMTVQKNFLSKMEKRRDSEGEVLRTAHRVDFIATYLGGLREQEKIKLESQ1 1109
Db      921  KVVMTVQKNFLSKMEKRRDSEGEVLRTAHRVDFIATYLGGLREQEKIKLESQ1 980
QY      1110  NYCSVLGSVADVLAQGGPRSGHCGESQVLAADHRCGLDGVOPGAGQPPSDT 1165
Db      981  NYCSVLGSVADVLAQGGPRSGHCGESQVLAADHRCGLDGVOPGAGQPPSDT 1030

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RESULT 8

Q7TFL4

ID Q7TFL4

AC Q7TFL4

DT 01-OCT-2003 (Tremblrel. 25, Created)

DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Transient receptor potential cation channel subfamily M member 5.

OS Mus musculus (Mouse).

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OC      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxID=10090;
RP      [1]
RC      SEQUENCE FROM N.A.
RC      STRAIN=129/Svx57BL; TISSUE=Testis;
RX      MEDLINE=22726392; PubMed=12842017;
RA      Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT      "TRP5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
RT      Selective Cation Channel.";
RL      Curr. Biol. 13:1153-1158(2003).
DR      EMBL; AY280365; AAP44477.1; -.
KW      Receptor.
SQ      SEQUENCE 1000 AA; 112459 MW; B5107610176B6660 CRC64;

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Query Match      71.5%; Score 4354.5; DB 11; Length 1000;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 842; Conservative 53; Mismatches 92; Indels 11; Gaps 4;

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QY      1  MODVQPRPGSPGDAEDRELGHRCEVNFSGGKRGKRVVPVSGVAPSVLFDLLAEW 60
Db      1  MQTTQSCGSPDPTEDGWEPILCRGEINFGSGKRGKRVVPVSGVAPSVLFDLLAEW 60
QY      61  HLPAPNLVSVLGEEOFPAMKSWLRDLVRKGLVKAQAQSTGAWILTSALRVGLARHVGOAV 120
Db      61  HLPAPNLVSVLGEERPLAMKSWLRDLVRKGLVKAQAQSTGAWILTSALRVGLARHVGOAV 120
QY      121  RHSLASTTKVRVAVAGMASLGRVLHRRILE--EAQEDFPVHYPPDDGGSGQPLCSLDS 178
Db      121  RHSLASTTKIRVAVAGMASLGRVLHRRILE--EAQEDFPVHYPPDDGGSGQPLCSLDS 180
QY      179  NLSHFTLVEPPGPGKG-DGLTELRLKHLKHSRAGYGTGSIEIPVLCVLLVNGDPNLT 237
Db      181  NLSHFTLVEPPGPGKG-DGLTELRLKHLKHSRAGYGTGSIEIPVLCVLLVNGDPNLT 240
QY      238  ERISRAVEQAAPWLLIAGSGGIADVLAAVLPKVAEKQKPEKPSKHFSEMEDIV 297
Db      241  ERISRAVEQAAPWLLIAGSGGIADVLAAVLPKVAEKQKPEKPSKHFSEMEDIV 300
QY      298  RMTKLLONTTSHOHLITVYDFEQQSEELDTVILKALVKACKSHSQEPQDYDELKLA 357
Db      301  HMTLQNTTSHOHLITVYDFEQQSEELDTVILKALVKACKSHSQEPQDYDELKLA 360
QY      358  WDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLVDNGADVADFLTYGRLO 417
Db      361  WDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLVDNGADVADFLTYGRLO 420
QY      418  LYRSVRSKSLFLDLQRKQEEARLTLAGLGTQAREPPAGPPAFSLHVSRLVLDKPDOD 477
Db      421  LYHSVRSKSLFLDLQRKQEEARLTLAGLGTQAREPPAGPPAFSLHVSRLVLDKPDOD 480
QY      478  CRGFTQDGRPGDRRAEKGPAKRPYTGOKWLLDNLNOKSENPMRDLFLWAVLQNRHEMATY 537
Db      481  CRGFTQDGRPGDRRAEKGPAKRPYTGOKWLLDNLNOKSENPMRDLFLWAVLQNRHEMATY 536
QY      538  WAMGEGVAAALAAACKILKEMSHLETEAEARATFAKVERLALDIFSECYNSSEARAP 597
Db      537  WAMGEGVAAALAAACKILKEMSHLETEAEARATFAKVERLALDIFSECYNSSEARAP 596
QY      598  LLVRNRCWSKTTCLHLATEADAKAFFAHGVQAFPLTRIMWGDMAAGTPIRLKLGAFCL 657
Db      597  LLVRNRCWSKTTCLHLATEADAKAFFAHGVQAFPLTRIMWGDMAAGTPIRLKLGAFCL 656
QY      658  ALVYTNLTTFSEAPLRTGLDLODLSLDTKESPLYGLQSRVELVEAPRAQGRGPRRA 717
Db      657  ALVYTNLTTFSEAPLRTGLDLODLSLDTKESPLYGLQSRVELVEAPRAQGRGPRRA 716
QY      718  VFLTRMRKFWGAPVTVFLGNVVMYFAFLFLTYVLLVDRPPQPGSGPEVTLFWFT 777
Db      717  VFLTRMRKFWGAPVTVFLGNVVMYFAFLFLTYVLLVDRPPQPGSGPEVTLFWFT 776
QY      778  LVLEIRQGFDTEDTHLVKFTLYVGNWNKCDMAIFIFIVGTCTMLPSAEPAGRTV 837
Db      778  LVLEIRQGFDTEDTHLVKFTLYVGNWNKCDMAIFIFIVGTCTMLPSAEPAGRTV 837

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Db 777 LVLEIRQGFDTEDTHLVKKFTLYVEDNNKCDMAIFLFIYGVTCRMVPSVFEAGTV 836
Qy 838 LAMDFWFTLRLIHI FAIHKQLGPKIIIVVERMKDVFFFLFSVWLVAYGVITQALLHP 897
Db 837 LAIDFWFTLRLIHI FAIHKQLGPKIIIVVERMKDVFFFLFSVWLVAYGVITQALLHP 896
Qy 898 HDGRLEWIFRVLRYPLVQLPGQIPLOEIDEARVNCSTHPLLLDSDSCPSLYANWLVIL 957
Db 897 HDGRLEWIFRVLRYPLVQLPGQIPLOEIDEARVNCSTHPLLLDSDSCPSLYANWLVIL 956
Qy 958 LLVTFLLVTNVLNLLIAMPSTYTFVQVGNADMFWKF 995
Db 957 LLVTFLLVTNVLNLLIAM-----FRVLTETGPMSTWYF 990

RESULT 9
Q8TD43 PRELIMINARY; PRT; 1214 AA.
AC Q8TD43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE cation channel TRPM4B (transient receptor potential cation channel
DE subfamily M member 4 splice variant B) (transient receptor potential
DE ion channel melastatin subgroup member 4 protein).
GN TRPM4B OR TRPM4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RA Perraud A.-L., Scharenberg A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22726392; PubMed=12842017;
RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT "TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
RT Selective Cation Channel.";
RL Curr. Biol. 13:1153-1158(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22791733; PubMed=12799367;
RA Nilius B., Prenen J., Droogmans G., Voets T., Vennekens R.,
RA Freichel M., Wissenbach U., Flockerzi V.;
RT "Voltage dependence of the Ca2+ activated cation channel TRPM4.";
RL J. Biol. Chem. 278:30813-30820(2003).
DR EMBL; AF497623; AAM18083.1; -
DR EMBL; AY297045; AAP44474.1; -
DR EMBL; AJ575813; CAB05941.1; -
DR Genew; HGNC:17993; TRPM4.
DR DR; GO:0016021; C:integral to membrane; IEA.
DR DR; GO:0005261; P:cation channel activity; IEA.
DR DR; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ionic channel; Receptor; Transmembrane.
SQ SEQUENCE 1214 AA; 134300 MW; 76ADA52690ED8F5 CRC64;

Query Match
Best Local Similarity 45.6%; Pred. No. 7.9e-182;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

Qy 26 GEVNFSGGKRGKFRVPSGVAPSVLFDLLIAEWHLPAPNLVSVLUGGEQPFAMKSWLR 85
Db 76 GELDTGAGRKHSNFRLSDRTPAAVYSLVTRTWGFRAPNLVSVLUGSGGPFVLTWLG 135
Qy 86 DVLRKGLVKAAGTGWILTSALRGLRHVGQAVRDHSLASTSTKRVVYVGMASLGRV 145
Db 136 DLLRGLVRAAGTGWAVITVGLTGTGRHVGVAVRDHQAATG-GTKVAVMGVAPWGVV 194

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Qy 146 LHRRIIEAAQEDFPVHY-----PEDDGGSQGLCSLDSNLSHFILTVEPBPBGKDGDTLTEL 200
Db 195 RNRDRTLINPKGSPARVWRGDPED--GVQFP---LDYNSAFELVDGTHGICLGGNRF 249
Qy 201 RLRLKHIISORAGYGGTGIETIPVLCILVNGDPTLIERISRAVEQAAPMLILVAGSGGIA 260
Db 250 RLRLSEYISQKGTGGTG-IDIPVLLLLIDGDEKMLTRIENATQAOPLCLLVAGSGGAA 308
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKFKSPKSHFSWEDIVRWTKLLQNTITSHOHL 313
Db 309 DCAETLED--TLAPGSGGARQGEARDIRIRFFPK-----CDLEVLQAQVERIMTRKELL 361
Qy 314 TVYDFEQEGSEELDTVLKALVKACKSHSQBPQDYLDLKLAVAMDVRDIAKSIIFNGDV 373
Db 362 TVYSSE-DGSEEPETIVLKALVKAC--GSSEASAYLDELRLAVAWNRVDAQSELFRGDI 418
Qy 374 EWKSCDLEEVWVDALVSNKBEFVRLFDVNGADVADFLTGYQLQELYSVSRSKSLDLDLQ 433
Db 419 QMRSFHLEASLMDALLNDRPEFVRLLSHGLSHGFLTPMKLAOLYGAAPSNLIRNLDD 478
Qy 434 RKQBEARLTLAGL--GTQOAREPPAGPPAFSLHEVSVRLKDFLQDACRGFTYQDGRPGDR 491
Db 479 QASHSAGTKAPALKGGAELRPP-----DVGHVRLMLKGMKCAPRYESGGAWDPH 528
Qy 492 RAEKGPAPKPTGQKWLDDLNQKS-----ENPWRDLFLWAVLQNRHEMATYFWAMQ 542
Db 529 -----PGQFGESWYLLSDKATSPSLDAGLQAPWSDLLWALLLRAQWAMTFWEMGS 583
Qy 543 EGVAALAAACKILKEMSHLETEAARATREA--KYRELALDLDFSECYSNEAFAFALLV 600
Db 584 NAVSSALGACILLRVMARLEPDABEAAARRKDLAFKFGMGVDLFGCEYRSRSEVRARULL 643
Qy 601 RNRCSWKTCLHLATEADAKAFHAGVQAFLTRIWMGDMAAGTPILRLGAFGLCPALV 660
Db 644 RRCPLWGDATCLQAMQADARAFQAQDGVQSILLTKQWGDWASTPIWALVLAFFCPPLI 703
Qy 661 YTNLITP--SSEAPLRTGLELDQLDLSLDTSEKSPLYQLQSRVEELVEAPRAQGD----- 712
Db 704 YTRLITFRKSEETREELE--FQMDSVINGEPVGTADPAEKTPLGVPYRSGRPGCGG 761
Qy 713 --RGPRAVFLITRWRKMGAPVTFLGNVNVYAFLEFLTYVLLVDFRPPPGPSGPEVT 770
Db 762 RCGRRRC--LRRFHFWGAPVTIFMGNVSVYLLFLFLFSRVLVDFQAP--PGSLELL 816
Qy 771 LYFWVFTLVLEBEIRQGFDTEDT-----HLVKKFTLYVGDNNKCDMAIFLFI 819
Db 817 LYFWAFTLLCELRQGLSGGSGSLASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCFL 876
Qy 820 VGVTCRMLPSAFAEAGRTVLAMDVWVFTLRLIHI FAIHKQLGPKIIIVVERMKDVFFFLFF 879
Db 877 LGVGCRLTFLGLYHLGRTVLCIDFMVFTVRLLIHIFTNKLQGLPKIVIVSKMKDKVFFFLFF 936
Qy 880 LSVMLVAYGVITQALLHEDHGRLEWIFRVLRYPLVQLPGQIPLOEIDEARV---NCSTH 936
Db 937 LGVMLVAYGVATEGLLRPRDSDPFSILRVRVTRPQLQIFGQIPQEDMDVALMEHNCNSE 996
Qy 937 PLLLEDSP-----SCPSLYANWLVILLVTFLLVTNVLNLLIAMFSTYTFVQVGNADM 991
Db 997 PGFWAHPPCAQAGTCVSYANWLVLLVIFLLVANILLVLLLIJANFSTYTFGKVGQNSDL 1056
Qy 992 FWKFORNLIYVEYHERPALAPPFILLSHLSLTLRRVFK-----EAEKHREHLED 1042
Db 1057 YWKAQRYLRIREFHSPALAPPFIVISHLRLRLQRCRRPRSPQSPSSPALEHFRVLSKE 1116
Qy 1043 LPDPLDQVWVWETVKENFLSKMEKRRDRSEGEVLRKTAHRVDFIATKVLGLIREQEKRI 1102
Db 1117 -----AERKLLTWESVHKENFLARADKRESERLKRSTQKVDLALKQLGHIREYEQRL 1172
Qy 1103 KCLESQINYCSVLVSSVADVLQAG-----GGP 1129
Db 1173 KVLREVOQCSVLGWVAEALSRALLPPGPG 1204

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RESULT 10
Q7TN37
AC Q7TN37 PRELIMINARY; PRT; 1213 AA.
ID Q7TN37
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Transient receptor potential ion channel melastatin subgroup member 4
DE protein.
GN TRPM4
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SVJ129; TISSUE=Heart;
RX MEDLINE=22791733; PubMed=12799367;
RA Nilius B., Prenen J., Droogmans G., Voets T., Vennkens R.,
RA Freichel M., Wissenbach U., Flockerzi V.;
RT "Voltage dependence of the Ca2+ activated cation channel TRPM4.";
RL J. Biol. Chem. 278:30813-30820(2003).
DR EMBL: AJ575814; CA05940.1; -.
KW Receptor.
SQ SEQUENCE 1213 AA; 135759 MW; E4959F53ED35FB66 CRC64;

Query Match 39.4%; Score 2399.5; DB 11; Length 1213;
Best Local Similarity 43.6%; Pred. No. 5.3e-178;
Matches 530; Conservative 185; Mismatches 343; Indels 157; Gaps 30;

QY 26 GEVFGGSGKRGKFRVPSGVAPSVLFDILLAEHLAPNLVSLVSGEEQPFAMKSWLR 85
DB 77 GDLDTYSYGRKHSNFLRLSDRTPATVYSIVSTRSGFRAPNLVSVLGGSGGPVLTWLQ 136
QY 86 DVLRLGLVKAAGSTGAWILTSALRLGLARHVGQAVRDHSLASTSTKRVVAVGMASLGRV 145
DB 137 DLLRRGLVKAAGSTGAWIVTGGIHTGIRHVGAVRDHQTASTGSS-KVAVMGVAPWGVV 195
QY 146 LHRRIIEAQEDFPVHY-----PEDDGGSGPLCLSLDNLSHFLNVEPVGPGKGLTEL 200
DB 196 RNRDLINPKGFPARYRWGDED--GVEFP---LDVNSAFFLVDDTGYTLGLGENRF 250
QY 201 RLRLKXHSIQEAGYGGTSGIPIVLCLVNGDPNLTIRISRAVEQAAPWLILVSGGIA 260
DB 251 RLRFESYVAQQTGVGGTG-IDIPVLLLLIDGDKMLKRIEDATQALPCLLVAGSGGA 309
QY 261 DVLAALVNGPHLLVP-----KVAEKQKFKPPSKHFWEDIVRWTKLLONITSHOHL 313
DB 310 DCLVETLED--TLAPSGGLRRGEARDIRRYFPK-----GDPVLQAQVIRIMTRKELL 362
QY 314 TVYDFEQEGSEELDTVILKALYKACKSHSOEPQDYLDELKLVAMDRVDIAKSEIFNGDV 373
DB 363 TVYSSE-DGSEFEFIVLRALVKAC--GSSEASAYLDELRLVAMNRVDIAQSEIFRGDI 419
QY 374 EWSKCDLEVMVDALVSNKPEFVRLVDNGADVFLTYGRLOELYSRSKSLFDLLQ 433
DB 420 QWRSFHLEASLDALNDRPEFVRLIISHGLSLGHFTLPVRLAQLYSVSPNSLRNLLD 479
QY 434 RQOEBEARLTLAGLTCQOAREPAG-----PAFSLHEVSRVLKDFLOACRGFY----- 482
DB 480 QASH-----ASSKSPVNGVTELRPP-----NVQVLRITLIGTCAPRYPARNT 524
QY 483 -----QDGRPGDRRAEKGPAKPTGQKWLIDLNQK-----SENPRDLFLVAVLQ 528
DB 525 RDSYLCQDREND-----SLMDWANKQPSDASFEQAFWSDLLIWAALL 569
QY 529 NRHEMATYFWAMQEGVAAALAAACKILKEMSHLETEAEAAATRE--AKYERLALDLFE 586
DB 570 NRAQWALYFWKSGNSVASALGACLLRVMARLESEAEAEARRKDLAATFESKVDLFE 629
QY 587 CYSNEARAFALLVNRNRCWSTTKTCHLATEADAKAFFADHGVQAFPLTRIWGDMAAGTP 646
DB 646

630 CYHNSEERARLLRRCLPLWGEATCQLAMQADARAFFAQGVQVSLLTQKMGEMDSTTP 689
647 ILRLIGAFCLPALVTNLTIFE--SEAPLRTGLELDQLDLSLDTKSPLYGLSRVEELV 704
690 IWallLAFFCPPLIYTNLIVFRKSEEEPTOKOLD--FDMDSINGAGPGPTVPSAKVAL 747
705 EAPRAQDGRGRAVFE---LLTRWKFGWAPVTVFLGNVVMYFAFLFTVTVLLVDFRPPP 761
748 E--RQRRPRGRALCGKSKSWDFWAPVTAFLGNVVSYLLFLLFAHVLVDFDQPTK 805
762 QGSPGPEVTLYFWVFTLVLEIRQGF-----FTDETHLVKFTLYYVGDNNKC 810
806 --PSVSELLYFWAFETLLCEELRQGLGGGWGSLASGGRGPDRAPLRHLHYLSDTNQC 863
811 DMVAIFLVGVTCMLPSAFEAAGRTVLAMDEWFTLRHLIHIHFAIHKOLGPKLIIVVERM 870
864 DLLALTCLFLGVGCRUTPGFLDGRVLCIDFMIFTLRLHLFTVANKOLGPKVIIVSKM 923
871 KDVFFFLFFLSVMLVAYGVTTQALLPHPHDGRLEWIFRRVLYRYPYLOIFGQIPLDEIDEAR 930
924 KDVFFFLFFLCLVWLVAYGVATGEGILRFPQDRSLPSILRRVYFAPYLOIFGQIPOEEMDVAL 983
931 V---NCS-----THPLLEDSP---SCPSLVANMLVILLVTLVTLVNLMLLIAMF 978
984 MIPGNCSEMERGSWAHP---EGPVAGSCVSYANMLVLLVLLVFLVANILLIAMIAMF 1039
979 SYTEQVVOGNADMFWKFORVNLIVVEHPRPALAPPILLSHLSLTIR-----RVFKK 1030
1040 SYTESKVHNSDLYWKAQRYSLIRFHSRPAAPPILIIISHVRLTGLKRLRCRCRANL 1099
1031 EAEHREHLERDLPPLOKVVTVETQKENTLSKMEKRRRDSGEVLRTKTAHRVDIFAK 1090
1100 PASPFVEHPRVCLSKAEERKLLTWSEVKENFLLAQARKRSDSERLARTSOXVDTALK 1159
1091 YLGRLREOKRIKLESQINYSVLVSVADVLAQGGPRSSQHCQEGSQLVAADHRGGL 1150
1160 QLQGREYDRRLRGLEREVHCGRSLVTWMAEALSH-----SALL----- 1198
1151 DQWEPQAGQPPSDT 1165
1199 ----PPGAPPPSPPT 1209

RESULT 11
Q96L84 PRELIMINARY; PRT; 1040 AA.
ID Q96L84
AC Q96L84;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TRP-related cation influx channel (Transient receptor potential cation channel subfamily M member 4 splice variant A).
DE TRPM4.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21438010; PubMed=11535825;
RA Xu X.Z.S., Moebius F., Gill D.L., Montell C.;
RT "Regulation of melastatin, a TRP-related protein, through interaction with a cytoplasmic isoform";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10692-10697(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22726392; PubMed=12842017;
RA Hofmann T., Chubanov V., Gudermann T., Montell C.;
RT "TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel.";
RL Curr. Biol. 13:1153-1158(2003).
DR EMBL: AY046396; AAL02142.1; -.
DR EMBL: AY297044; AAP44473.1; -.
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DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005261; F: cation channel activity; IEA.
DR GO: GO:0006812; P: cation transport; IEA.
DR DR INTERPRO: IPR002111; Cat_channel_TrpL.
DR DR INTERPRO: IPR005821; Ion_trans.
DR PFAM: PF00520; ion_trans; 1.
KW Ionic channel; Receptor; Transmembrane.
SQ SEQUENCE 1040 AA; 115565 MW; 684A8C554B2B0F2E CRC64;

Query Match 35.5%; Score 2184.5; DB 4; Length 1040;
Best Local Similarity 45.6%; Pred. No. 2.7e-161;
Matches 486; Conservative 156; Mismatches 320; Indels 111; Gaps 26;

QY 125 LASTSTKRVVAVGMAISGRVLRHRIIEEAQEDFPVHY-----PEDDGGSGQPLCLSDSN 179
DB 1 MASTG-GTKVAVGVAVGVVVRNDRDTLINPKGSPFARYRWGDPED--GVQFP---LDYN 54

QY 180 LSHFILVPPGPGKGDGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTLER 239
DB 55 YSAFLVDDGTHGCLGGENRFRLESYSQKGTGGTG-IDIPVLLLLIDGDEKMLTR 113

QY 240 ISRAVEQAAPWLLVVGSGGIADVLAAALVNQPHLLVP-----KVAEQKFEKPSKXFS 292
DB 114 IENATQAQLPCLLVAGSGGAADCLAEITLED--TLAPSGGARQGEARDIRRRFPK--- 167

QY 293 WEDIVRWTKLQNTITSHOHLITVYDFEQQSEELDTVLKALVACKSHSOEPQDYLDL 352
DB 168 -GDLEVLQAQVERIMTRKELLTVYSSE--DGSEEFETVLKALVKAC--GSSEASAYLDEL 223

QY 353 KLAVANRVDIAKSEIFNGDVNWKSCDLEFVNVDAVSNKEPFEVRLFDVNGADVADFLTY 412
DB 224 RLAVANRVDIAQSEIFNGDVNWKSCDLEFVNVDAVSNKEPFEVRLFDVNGADVADFLTY 283

QY 413 GRLQELYSVRSKSLPDLLOKQEEARLTLAGL--GTQQAQREPAGPAPFSLHEVSRL 470
DB 284 MRLAQLYSAAPSNLSIRLLDQASHSAGTKAPALKGGAELRPP-----DVGHVL 333

QY 471 KDFLQDACRGYQDGRPDRRRAEKGPAPKRTGTOKWLLDLNQS-----ENPWRDL 521
DB 334 RMLLGKMCAPYPSGGAWDPH-----PQGGFESNYLLSDKATSPSLDAGLGQAPWSDL 388

QY 522 FLWAVLQNRHEMATYFWANGQGVAAALAAACKILKEMSHLITEAARATREA--KYERL 579
DB 389 LLWALLNRAQMAYFWEMGNVSSALGACLLRVWALRPDABEAARRKDLAFKFGM 448

QY 580 ALDLFSECYNSSEARAFALLVRNRCWSKTTCLHLATEADAKAPFAHGVQAFTRIWWG 639
DB 449 GVDLFGECTRSSEVRAELLRRCPWGDATCLQAMQADARAFPAQGVQSLITQKWWG 508

QY 640 DMAAGTPTILRLGAFPLCVYTNLITF--SEAPLRTGLEDLQDLSDTEKSPLYGLQ 697
DB 509 DMASTPTIWLALVAFCCPLIYTRLTITFKSEEEPTREELE--FQMSVINGEGVGTAD 566

QY 698 SRVELVEAPRAQD-----RGPRAVFLTRWRKFWGAPVTVFLGVNVYFAFLF 749
DB 567 PAEKTPLVGPVRSRPGCGGRCGRRC---LRRWFHFGAPVTTFMGNVSYLLFLFLF 623

QY 750 TVLLVDFPRPPQPGSGPEVTLYFWVFTLVLEIEIRQGFTEBDT-----HLVKK 798
DB 624 SRVLLVDFOQAP--PGSELELLYFWAFILLCELRQGLSGGGGSLASGPGPGHASLSQR 681

QY 799 FTLVYGDNNKCDMVAIFLVIGVTCRMLPSAFEAGRTVLAMDFWFTLRLIHFAIHQ 858
DB 682 LRLYLADSWNCDLVALTCFLGVGCRUTPGLYHLGRVLCIDFVWFTVRLIHIFVANK 741

QY 859 LQPKLIIVERMKWVFFFLFSLVWLVAVGVTTQALLHPHDCGLEMIFFRVLYRYLOIF 918
DB 742 LGPKIVIVSRMKWVFFFLFSLVWLVAVGVATEGLLRDRSDPFSILRRVRYRYLOIF 801

QY 919 GOIPLEIDEARV--NCSTHPLLEDSP-----SCPSLYANWLVILLIVTELLVTVNVL 970
DB 802 GQIPQEDMDVALMEHNSCSSEFGFWAHPPGAQAGTCVQYANWLVILLIVTELLVANILL 861
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Db	334	RMLGKMCAPRYPGGAWDPH-----PGQFGESMYLLSDKATSPSLDAGLGQAPWSDL	388
QY	522	FLWAVLQNRHETATYFWAQEGVAAALAAKILKEMSHLETEAEAAARATREA--KYERL	579
Db	389	LLWALLNRAQAMWYFWGNSVAVSALGACLLLRVWARLEPDABEAARKDLAFKFEW	448
QY	580	ALDLFSECVSNGEARFALLVRNRCSKTTCLHLATEADAKAFFAHGQVQAFPLRIWKG	639
Db	449	GVDLFGEVSRSEVRAARLLRRCLPLWGDCATCLQAMQADARAFFAQQDGVQSLLTQKMG	508
QY	640	DNAAGTPIRLICAFPCALVYNLTIF--SEAPLRTGLELDLQDLDLSTKSPYGLQ	697
Db	509	DNASTPIWALVLAFFCPPIYTRLTFRKSEEPREELE--FDMDSVINGEPPGTAD	566
QY	698	SRVEELVEAPRAQCD-----RGPRAVFLTRMRKFWGAPVTYFLGNVVMYFAFLFLF	749
Db	567	PAEKTPLGVPRQSGRCGCCGGRRC--LRWFHFWGAPVTIPMGNNVSYLLFLFLF	623
QY	750	TYVLLVDFRPPQGGSPGVTVYFWVFTLVLEIRQGFTEBDT-----HLVKK	798
Db	624	SRVLLVDFQAP--PGSLBLLYFWAFTLLCBELRQLSGGGGLASGGPGPGHASLSQR	681
QY	799	FTLYVGDWNNKDMVAIFIVGTCRMLPSAFEAGRTVLADPMVFTLRLTHIPAIHQ	858
Db	682	LRLLYLDASNQCDLVALTCFLGCVGCLRTPGLYHLGRVLCIDFMVFTVLLHIFTVVKQ	741
QY	859	LGPKIIVBRMMKDVFFFLFVSVLVAYGVVTOALLPHDGRLEWIFRVLRYRPLYQIF	918
Db	742	LGPKIVIVSKMKDVFFFLFVSVLVAYGVVTOALLPHDGRLEWIFRVLRYRPLYQIF	801
QY	919	GOIPLDIDEARV--NCSTHPLLEDSP-----SCPSLYANWLVILLVITVLLVNVLL	970
Db	802	GOIPQDMVDVMEHNSCSSEPGFAHPPGAQAGTCVSYANWLVILLVITVLLVNVLL	861
QY	971	MNLLIAMSFTYTVQVGNADMKQRYNLVIEYHERPALADPFLLSHLSLTLRVPFK	1030
Db	862	VNLLIAMSFTYTVQVGNADMKQRYNLVIEYHERPALADPFLLSHLSLTLRVPFK	921
QY	1031	-----EAEHREHLERDLPDQKQVWETVKENFLSKMKRKRDRSEGEVLRKT	1081
Db	922	PRSPQSSPALHEFRVYLSKE-----AERKLLTWESVHKENFLARARAKRDSERLRT	977
QY	1082	AHRVDFIAKYLGLRQEKRIKLSQINYS	1113
Db	978	SQKVDLALQGHIREYQRLKVLREVOQCS	1009
RESULT 13			
ID	Q7Z5D9	PRELIMINARY;	PRT; 1069 AA.
AC	Q7Z5D9;		
DT	01-OCT-2003 (trEMBLrel. 25, Created)		
DT	01-OCT-2003 (trEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (trEMBLrel. 25, Last annotation update)		
DE	Transient receptor potential cation channel subfamily M member 4		
DE	splice variant C.		
GN	TRPM4.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22726392; PubMed=12842017;		
RA	Hofmann T., Chubakov V., Gudermann T., Montell C.;		
RT	"TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent		
RT	Selective Cation Channel."		
RL	Curr. Biol. 13:1153-1158 (2003).		
DR	EMBL; AY297046; AAP44475.1; --		
KW	Receptor.		
SQ	SEQUENCE 1069 AA; 118629 MW; 80DEBD935A55F200 CRC64;		
Query Match			
		34.4%;	Score 2098; DB 4; Length 1069;
Best Local Similarity 41.2%; Pred. No. 1.6e-154;			
Matches 475; Conservative 157; Mismatches 303; Indels 218; Gaps 24;			
QY	26	GEVNFSGSKKGGKFRVPSGVAPSVLFDLLIAEHLPAENLVSVLVGSEQPFAMKSWLR	85
Db	76	GELDTGAGRKSNFLRLSDRTPAAYSLVTRTWGFRAPNLVSVLVGSGGVPRLQWLQ	135
QY	86	DVLRKGLVKAQOSTGAWILTSALRVGLARHGOAVRDHSLASTSTKRVVAVGMAISGRV	145
Db	136	DLLRGLVRAAOSTGANIVTGLHGTIGHVGVAVRDHOMASTG-CTKVAVGVAVPWVV	194
QY	146	LHRRILEEAQEDPPVHY-----PEDGGSGQGLCSLSDSNLSHFILVEPPGPKGDGLTEL	200
Db	195	RNRDITLNPKGSFPARYRWGDPED--GVQFP--LDVNSAFFLVDDCTHGLCGENRF	249
QY	201	RRLKHLHSEORAGYGGTGSIEIPVCLLVNGDPNTLERISRAVEQAAPWLLVVGSGGTA	260
Db	250	RURLSEYSIQQTGVGGTG-IDIPVLLLLIDGDKMLTRIEATQALPCLLVAGSGGAA	308
QY	261	DVLAALVNPQHLVLP-----KVAEKQPKFPSPKHSFMSWEDIVRWTKLONITSHOHL	313
Db	309	DCIAETLED--TLAPSGGARQGEARDIRREFPK-----GDLEVLQAVRIMTRKELL	361
QY	314	TYDPEQEGSEELDTVILKALYKACKSHSQEPQDYLDLKLAVAMDVRDVIASKEIFNGDV	373
Db	362	TVYSSE-DGSEBEFETIVLKVKAC--GSSEASAVLDELRLAVAMRVVDIAQSELFRGDI	418
QY	374	EWKSCDLEEVVVDALVSNKPEFVRLFDVNDGADVADPFLTYGRLOELYSRVRKSLLDLQ	433
Db	419	QWRSHLEASLMDALNDRPEFVRLISHGLSHGLFTPMRLAQLYSAAPSLSLRNLAD	478
QY	434	RKQBEARLTLAGL--GTQAREPPAGPAPAFSLHYSRVLKDFLQACRFGYQDGRGRR	491
Db	479	QASHAGIKAPALKGGAELRPP-----DVGHVLRMLLKKMCAPIRYSGGAWDPH	528
QY	492	RAEKGPAPKPTQKQWLLDNLNKS-----ENPWRDLFLWAVLQNRHETATYFWAQ	542
Db	529	-----PGQFGESMYLLSDKATSPSLDAGLQAPWSDLLIALLNRAQAMYFWMG	583
QY	543	EGVAAALAAACKILKEMSHLETEAEAAARATREA--KYERLALDLFSECVSNGEARFALL	600
Db	584	NAVSSALGACLLRVMARLEPDABEAARKDLAFKFEWGVDFLFGECYRSRSEVRAARLL	643
QY	601	RNRCSKTTCLHLATEADAKAFFAHGQVQAFPLRIWGDMAAGTPILRLICAFPCALV	660
Db	644	RACPLWGDCATCLQAMQADARAFFAQQDGVQSLLTQKMGDMASTTPIWALVLAFFCPPI	703
QY	661	YTNLTIP--SEAPLRTGLELDLQDLDLSTKSPYGLQSRVEELVEAPRAQDGRGPRAV	718
Db	704	YTRLITFRKSEEPREELE--FDMDSVINGEPP-----	735
QY	719	FLTLTRKFWGAPVTYFLGNVVMYFAFLFITYVLLVDFRPPQPGSPGPEVTLYFWVFTL	778
Db	736	-----	735
QY	779	VLEIRQGFTEBDTHLVKKTLYVGDWNNKDMVAIFLIVGTCRMLPSAFEAGRTVL	838
Db	736	-----VGLT-----PGYHLQRTVL	750
QY	839	AMDFMVFTLRLTHIPAIHQKLGPKIIVVERMMKDVFFFLFVSVLVAYGVVTOALLHHP	898
Db	751	CIDFMVFTVRLHIFTVANKQLGPKIVIVSKMKDVFFFLFVSVLVAYGVVTOALLHHP	810
QY	899	DGRLEWIFRVLRYRPLYQIFQIPLDEIDEARV--NCSTHPLLEDSP-----SCPSLY	950
Db	811	DSDFPSILRRVYRPLYQIFQIPLQEDMDVAMEHNSCSSEPGFAHPPGAQAGTCVSY	870
QY	951	ANWLVLLVITVLLVNVLLIAMSFTYTVQVGNADMKQRYNLVIEYHERPAL	1010
Db	871	ANWLVLLVITVLLVNVLLIAMSFTYTVQVGNADMKQRYNLVIEYHERPAL	930
QY	1011	APPFILLSHLSLTLRVPFK-----EAEHREHLERDLPDQKQVWETVKEN	1061


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DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00520; ion trans; 1.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00092; N6_MTASE; 1.
KW Ionic channel; Receptor; Transmembrane.
FT NON_TER 1507 1507
SQ SEQUENCE 1507 AA; 172364 MW; 86E552DE25939785 CRC64;

Query Match      33.2%; Score 2021; DB 11; Length 1507;
Best Local Similarity 39.1%; Pred.No. 2.9e-148;
Matches 449; Conservative 193; Mismatches 386; Indels 120; Gaps 22;

QY 26 GEVNFQSGGKRGKFRVPSGVAPSVLFDLLAEWHLPAFNVLVSLVGEQPFAMKSWLR 85
Db 127 GDIVFTDLQKGVKYYRVSDTPESSVIYQLMTQHWGLDVPNLLISVTGAKNFNMKLRLK 186
QY 86 DVLRLKGLVKAQSTGAWILTSALRUGLARHVGQAVRDHSLASTSTKRVVAVMGASLGRV 145
Db 187 SIFRRGLVKAQTTGAWIITGGSHTGVMKQVGVAVRDFSLSSCKEGETITIGVATWGTI 246
QY 146 LHRRILEEAEQEDPPVHYHEDDGGSGQPLCLSDNLSHFILVEPPGPKGDGLTELRLLE 205
Db 247 HNRGLIHPMGFPAYMLDEEG-QGNLTCLDSNHSHFILVDDGTGQYGVETPLRTKLE 305
QY 206 KHISEQAGYGGTGSIEIPVLCLLVNGDENTLERISRAVEQAAPWLILVSGGGIADVLAA 265
Db 306 KFISEQTKERGGV-ALKIPICVVLGGPGTTLHTIYNAINNGTGPCVIVEGSGRVADVIAQ 364
QY 266 LVNQP--HLLVPKAEKQ---FKEKFPKSHFSEWIDIVRTKLLQNTITSHQLLTIVYDFEQ 320
Db 365 VATLPVSEITISLIQOKLSIFFQEMFET--FTENQIVEMTKTQDIVRRRQLTTIFREGK 422
QY 321 EGSEEDLTVILKALVKACKSHQEPDQYLD-ELKLAVAMDVRDIAKSEIFNGDVEMKSD 379
Db 423 DQODVDVAILQALLKASRSQDFHGENWDHQLKAVANRVDIARSEIFTDEWQKPAD 482
QY 380 LEEVMVDALVSNKPEFVRLFDVNGADVADPLTYGRQLQELYSVSRKSLFLDLIQR-KQEE 438
Db 483 LHPMTAALISNKPFEFVRLFLENGVRLKEFVMTDTLLCLYENLEPSCLFHSLKQLKVLAE 542
QY 439 ARILTLAGLTQQAPEPPAGPAPFSLHEVSRVLKDFLODACRGFYQDGRPGDRRRAE---- 494
Db 543 QRLAYA-----SATPRIHMHVAVQLRELLGDSQTLLYPYPRVYTDPRLSMTVP 591
QY 495 -----KGPAPKPTGO-KWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWAMGQ 542
Db 592 HIKLVQGVSLRSLYKRSTGHVFTFD-----PVRDLIWAIVQNHRELAGIITWAQSQ 644
QY 543 EGVAAALAAACKILKEMSHLE--TEAFAARATREAKYERIALDLFSECYNSSEARAFALIV 600
Db 645 DCTAAALACSKILKELSKEEDTDSSEEMALADEFEHRAIGVFTCYRKDEERAQKLIV 704
QY 601 RNRRCWSKTTCLHLATEADAKAFFAHDGVOAFLTRIWDGMDAAGTPIILLGLAFLCPALV 660
Db 705 RVSEAMGKTTCLQLALEAKDMKFVSHGGIQAFLTKVMWGQLCVDNGLNRIILCMLAFPLL 764
QY 661 YTNLITFSEAPLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
Db 765 FTGFTISFREK-----RQALCRPARV----- 785
QY 721 LTRWRKFWGAPVTVFIGNVVMYPAFLFTYVLLVDPRPPQPGSPGEVTLXFWVFTVLV 780
Db 786 ----RAFFNAPVVFHNMILSYFAFLCLFAYVLWVDFQP---SPSWCEYLIIVLWLPFLVC 838
QY 781 EEIRQGFPTDED--THLVKFTLYVGNWNKCDWVAIFLFIQVTCRMLPSAFEAGRTVLA 839
Db 839 EETRYLFYDPPDGGCLMKMASLYFSDFWNKLVDGAILFIVGLTCRLIPATLYPGRIILS 898
QY 840 MDMFMVFTLRIHTFAITHKOLGPKIIVVERMKDVRFEFLFSLVWLVAYGVTTCALLPHD 899
Db 899 LDFIMECLMHLFTISKTLGPKRIIIVKRMKDVFFFLFLLAVWVSVFGVAKQAILIHN 958
QY 900 GRLEWIFRRVLRPYLIQFIQIP--LDEIDEARVNCs---THPLILLEDSFSCPS----- 948
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Search completed: September 14, 2004, 00:06:08
Job time : 77 secs

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Db 959 SRVDMIFRGVWVHSYLTIFGQIPTIYIDGVNFSDMQSPNGTDY-----KPKCESDWTGQ 1014
QY 949 --LYANWLIVLLLVTELLVTNVLNMLLIAMPSYTFQVVOGNADMFWKFORYNLIVEYHE 1006
Db 1015 APAPPEWLTVTLLCLYLLFANILLNLLIAMFNFTQEOEHTDQIWKFORHDLIBEYHG 1074
QY 1007 RPAALAPPFILLSHLSLTLRVFKKEAEKREHLERDLPDLDQKVVTWETVQKENFLSKM 1066
Db 1075 RPAPPPLILLSHLQLLIRIVLIPAKRHQKUNKLENEETALLUSWELYLKENYILQNG 1134
QY 1067 EKERRDSEGEVLRKTAHRVDFIAKYL-----GGLREQEKRICKLESQINYSGLVSSV 1119
Db 1135 QYQOKQRPQKIQDISSEKVDITWVDLLDMQVKRSGSTEQ--RLASLEEQVTVTRALHWI 1192
QY 1120 ADVLAQGG 1127
Db 1193 VTTLKDSG 1200
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 14, 2004, 00:03:08 ; Search time 23 Seconds
(without alignments)
2614.968 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence: 1 MDVQGPFGSPGDAEDRR.....HRGLDGEQPGAGPPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/2/aaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/aaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/aaa/6A_COMB.pep:*

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5: /cgn2_6/ptodata/2/aaa/PTCUS_COMB.pep:*

6: /cgn2_6/ptodata/2/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2039	33.5	1503	US-09-600-087-2	Sequence 2, Appli
2	1566.5	25.7	1095	US-09-112-096-15	Sequence 15, Appli
3	1566.5	25.7	1095	US-09-636-215-778	Sequence 778, App
4	1566.5	25.7	1095	US-09-685-166A-778	Sequence 778, App
5	1558.5	25.6	1095	US-09-636-215-780	Sequence 780, App
6	1558.5	25.6	1095	US-09-685-166A-780	Sequence 780, App
7	1240.5	20.4	1533	US-08-623-679-9	Sequence 9, Appli
8	1240.5	20.4	1533	US-08-933-774-9	Sequence 9, Appli
9	1240.5	20.4	1533	US-09-181-030-9	Sequence 9, Appli
10	1240.5	20.4	1533	US-09-534-242-9	Sequence 9, Appli
11	1240.5	20.4	1533	US-09-454-854-9	Sequence 9, Appli
12	1240.5	20.4	1533	US-09-164-671-9	Sequence 9, Appli
13	1162.5	19.1	1497	US-08-623-679-7	Sequence 7, Appli
14	1162.5	19.1	1497	US-08-933-774-7	Sequence 7, Appli
15	1162.5	19.1	1497	US-09-181-030-7	Sequence 7, Appli
16	1162.5	19.1	1497	US-09-534-242-7	Sequence 7, Appli
17	1162.5	19.1	1497	US-09-454-854-7	Sequence 7, Appli
18	1162.5	19.1	1497	US-09-164-671-7	Sequence 7, Appli
19	820	13.5	315	US-09-020-956-112	Sequence 112, App
20	820	13.5	315	US-09-030-607-112	Sequence 112, App
21	820	13.5	315	US-09-439-313-112	Sequence 112, App
22	820	13.5	315	US-09-352-616A-112	Sequence 112, App
23	820	13.5	315	US-09-232-149A-112	Sequence 112, App
24	820	13.5	315	US-09-159-812-112	Sequence 112, App
25	820	13.5	315	US-09-636-215-112	Sequence 112, App
26	820	13.5	315	US-09-685-166A-112	Sequence 112, App
27	820	13.5	315	US-09-115-453-112	Sequence 112, App

Sequence 112, App
Sequence 818, App
Sequence 818, App
Sequence 11, Appli
Sequence 378, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 175, App
Sequence 175, App
Sequence 33, Appli
Sequence 6, Appli
Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-09-600-087-2

; Sequence 2, Application US/096000087

; Patent No. 6548272

; GENERAL INFORMATION:

; APPLICANT: Shimizu, No. 6548272uyoshi

; APPLICANT: Nagamine, Kentaro

; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN

; FILE REFERENCE: 11283-004001

; CURRENT APPLICATION NUMBER: US/09/600,087

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: PCT/JP99/06289

; PRIOR FILING DATE: 1999-11-11

; PRIOR APPLICATION NUMBER: JP/321200/1998

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1503

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: TRANSMEM

; LOCATION: (320)...(344)

; NAME/KEY: TRANSMEM

; LOCATION: (750)...(773)

; NAME/KEY: TRANSMEM

; LOCATION: (794)...(818)

; NAME/KEY: TRANSMEM

; LOCATION: (867)...(891)

; NAME/KEY: TRANSMEM

; LOCATION: (900)...(924)

; NAME/KEY: TRANSMEM

; LOCATION: (932)...(956)

; NAME/KEY: TRANSMEM

; LOCATION: (1024)...(1048)

US-09-600-087-2

Query Match

Best Local Similarity 33.5%; Score 2039; DB 4; Length 1503;

Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGSKRGKFKVRVPSGVAPSLFDLLAHLPAFNLVSLVGEQPFAMKSWLR 85

DB 128 GDIVFTGLSQKVKVVRVSDPTSPSVIHLMTQHWGLDVPNLLISVTGAKFNMKPRLK 187

QY 86 DVLRLGLVKAAGSTCAWILTSALRVGLARHVQAVRDHSLASTSTKVRVAVGVMSLGRV 145

DB 188 SIFRRGLRVKAQTGTGAWITGSHSTGVNMQVGEAVRDFSLSSSYKEGLITIGVATWGTV 247

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146 LHRRLIEEAQDFVHPVDPEDGGQGPLCSLSDSLSHFVLVPEPPGKGDLGLTELRLE 205
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248 HRREGLIHTPSFFAAYILDEBG-QGNLTCLDSNHSFILVDDGTHGQYGVIEPLRLE 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
206 KHISEORAGYGTGSIETPVCLLVGNDPNTLIERISRAVEQAAPWLILVSGGADVLAA 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307 XFISEQTKERGCV-AIKPIVCVVLGGGPGTLTIDNATTNGTFCVVVEGSGRADVIAQ 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
266 LVNOP--HLLVPKVAEQ--FKEKPSKHSWEDIVRWTLLQNTSHOHLTYVDFEQ 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
366 VANLPVSDITISLTOQLSVFQEMFET--FTESRIEWTTKIQIDVRRRQLLVFRGK 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
321 EGSEELDTVILKALVKACKSHSQBPQDYLDELKLAWDRVDIAKSFINGDVWKSCD 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
424 DQOQDVDAIQLLAKASRQDHFCHENWDLKLAWANRVDIARSBIFMDEWQKPSD 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
380 LEEVMDALVNKPEFVPLFVNDGADVADFTYGLQELYSVSKSLFLDQLQKQBEA 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
484 LHPTMTAALISNKPEFVKFLFENGVLKEFVTWDTLLYENLDPSCLFHSKLOK---- 538
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
440 RLTLAGLGTQARBPAPG--PAFSLHEVSRLVLDKQACKGFYQDGRGPRDRR----- 492
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539 -----VLVEDPERPACAPAPRLQMHVAVQLRELLGDTQPLYPRHNDRLRLLPV 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
493 -----AEKGPAKPTQKWLDDLNQKSNPWRDLFWAVLQNRHEMATYFWAMQ 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
593 PHVKLVQGVSLRSLYKSSGHVTF-----TMDPIRDLIIWAIQNRRELAGIWAQSQ 646
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543 EGVAALAAACKILKEMSHLETAEAR--ATRAKYERLALDLFSECVSSEARAFALL 599
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
647 DCIAAALACSKILKELSEEDTSSSEMLALAE-EYEHRAIGVFTECYRDXDEERAQKLL 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
600 VRRNRCMKTCLHLATADAKAFPAHDGVQAFTRIWMGDMAAGTPTLRLGLAFLCPAL 659
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706 TRVSEAWGKTTCLQALEAKDMKPVSHGGIOAELTKVWVGQLSVNDGLWRVTLCLMPL 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
660 VYTNLITSEAPLRTGLEDLQDLSLDTSEKPLVGLQSRVEELVEAPRAGDGRPAVF 719
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766 LLTGLISPRKR-----LQD-----VGTFAA----- 786
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720 LLTWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGSEVTLFYWFVTLV 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
787 ---RARAEFTAPVVVHNLISYFAFLCLFAYLWMDVQPV---PSWCECAIYLMFLSLV 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
780 LEEIRQGFDTDETHLVKKFTLYVGDNNKCDMAIFLFIYGVTCRMLPSAFEAGRTVLA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
841 CEEMRQLFVDPDECGLMKKAALYFSDFNKLDVGAILLVAGLTCRLPATLTPYGRVILS 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
840 MDPVFTLRLTHIFAIHQKGPKLIIVERNMKDVFFLFFLSVWLVAYCVTTQALLHPHD 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
901 LDFILFCRLMHIFTISKTLPKLIIVKRNKMDVFFFLFLAVVWVSGVAKQAILHNE 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
900 GRLEWIFRRLVRYPLQIFGQIP--LDBIDEARVNCS--THPILLEDSPSCPS----- 948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
961 RRVWLFRGAYVHSLTIFGQIPGYIDGNVFNPECHSPNGTDPY----KPKCPSDATQ 1016
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
949 ---LYANWLVILLVTLVNTVLLMNLIIAMFSYTFVQVQGNADMPKFWQRYNLIVEYHE 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1017 RPAPPEWLVLLCLLYLFTNILLNLLIAMFNVTYFQVQBHTDQIKWQFQRHDLIEEYHG 1076
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1007 RPALAPPILLSHLSLTLRRVPKAEKREHLERDLDPDLQKVVWETVQENKFLSKM 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1077 RPAAPPFILLSHLQFLFTKRVVLKTPAKRHKQLKNKLEKNEALLSWEIYLKENYLNQR 1136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1067 EKRARDSGEVLKRTAHRVDFTAKYL-----CGLREQEKRIKLESQINYSVLVSS 1118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1137 QFOQKQREKIEDISNKVDAMVDLLDPLKRSQSM---BQRLASLEEQAQARALFW 1193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1119 VADVLAAQGGRRSSQHCCEGSQLVAAD---HRGGLDGWBPQ 1157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1194 IVRTLRSQFSSEADVPTLASQAAAEPEPDAEPGRKTEEPG 1235
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```
RESULT 2
US-09-112-096-15
; Sequence 15, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reinher Laus
; APPLICANT: Michael H. Shaper
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; TITLE OF INVENTION: Antigen Compositions
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112,096
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056,110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-112-096-15

Query Match      25.7%; Score 1566.5; DB 3; Length 1095;
Best Local Similarity 34.3%; Pred. No. 2.2e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

QY 26  GEVNFSGGKKRGKGFVPSGVAPSVLFDLLLAELWHLPAFNLVSVLVEEQPFAMKSLR 85
DB 95  GDIOFETLGGK-GKVIKSLCDDTDAEILYELLTQHHLKTPNLVSVTGVAKNFALKPMR 153
QY 86  DVLKGLVKAQOSTGAWILTSALRVGLARHVQAVRDSHSLASTSTKRVVAVGVASLGRV 145
DB 154 KIFSR-LIYTAQSKGAWILTGGTHYGLTKYIGEVVRDNTI--SRSEENIVAGIAAGMV 211
QY 146 LHRILE---BAQEDFPVHYPEDGGQGPLCSLSDSLSHFVLVPEPPGKGDLGLTEURL 202
DB 212 SNRDTLRNCDAGFYLAQYLMDD-FTRDPLIYLDNNHHTHLLLVNDGCHGHTPEAKURN 270
QY 203 RLEKHISE---QRAGYGGTGSIEIPVLCVLVNGDPNTLIERISRAVEQAAPWLILVSGGI 259
DB 271 QLEKHISERTIQDSNYG---KIPVCFAGGGGKETLAKINTSIKNKPCVVVEGSGRI 326
QY 260 ADVLAALVNQPHLLVPKVAEKQFKEKFPF--KHSWEDIVRWTLLQNTSHOHLTYVD 317
DB 327 ADVIASLVEVBDAPTSSAVKEKLVRFPLRTVSRLSSEETESWIKWLKEILCSHLLTVIK 386
QY 318 FEQSGSELDTVILKALVKACKSHSQBPQDYLDELKLAWDRVDIAKSEIPNGDVWKS 377
DB 387 MEEAGDEIVSNAIYALYKAFSTSEQDKNNWGQLKLEWNLQDLDEINFTNDRWES 446
QY 378 CDLEVMVDALVSNKPFVRLFVNDGADVADFTYGLRQLQELYSVSRKSLFDLLQ---R 434
DB 447 ADLQEVMTALIKDRPKFVRLFLEGNLNRKFLTHDVLTELF--SNHFTSLVYRNLIQAKN 505
QY 435 KQEARLUTLAGLGTQARBPAPGPAFSLHVSRLVLDKQACKGFYQDGRPG--DRRRA 493
DB 506 SYNDALLTF-----VWKLVANFR---RGRFRKDRNGRDEMDI 539
QY 494 EKGPAKPTGQKWLDDLNQKSNPWRDLFLWAVLQNRHEMATYFWAMQEGVAAALAAACK 553
DB 540 E-----LHDVSPITRHPQLALFIWAILQNKKELSKVIWEQTRGTGTLAALGASK 587
QY 554 ILKEMSHLETBAEAAATREA--KYERIALDLFSECVSSEARAFALVRRNRCMKTTC 611
DB 588 LLKTLAKVNDINAAGESEELANEVETRAVELFTECYSSDEDLAEQLLVYSCAAMGSGNC 647
QY 612 LHLATEADAKAFFADGVQAPLTIWGDMAAGTPIRLGLAFLCPALVYTNLITFSEEA 671
DB 648 LELAVEATDQHTAQPGVQNFSLSKQWYGETSRDTKNWKIILCLFTIPLVGGGFSFRKK- 706
QY 672 PLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDGRPAVFILTRWRKFWGAP 731
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Db 707 -----PVDKHK-----LLWYVAFFTSP 725
Qy 732 VTVFLGNVYFAFLFTVLLVDRPPPGSGPEVTLYFWVFTLVLEETROGFFTDE 791
Db 726 FVFSNWNVYFAFLFLFAVLLMDHFSVPH-----PPELVLSLVFLFCDEVRQWTVNGV 782
Qy 792 DTHLVKKFTLYVGDNNKCDMAIFLFIIVGVTCTM-----LPSAFEAGRTVLAMDVMVFTLR 848
Db 783 N-----YFTDLNWNMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLR 833
Qy 849 LTHIFAIHKQLGPKIIVVERMMKDVFFFLFSLVNLVAVGTVTQALLHPHGRLEWIFRR 908
Db 834 LTHIFTVSRNLGPKIIMQLMLIDVFFFLFSAVNVAFVARQGLRQNEQSRWIFRS 993
Qy 909 VLYRPYLOIFGOIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLYANWLVLILL 959
Db 894 VIYEPYLAIFMGQVPSD-VDGTTTDFAHCTFTGNEKPLCVELDEHNLPR-FPEWITIPIV 951
Qy 960 VTFLLVTVNLLMNLIAFMSYTFQVVGADMFVKFORVNLVIEYHERPALAPPTLLSH 1019
Db 952 CIYMLSTNILLNVLVAMFGYTVGVQENNDQVWKFQRYFLVQVYCSRLNIPFPFIVPAY 1011
Qy 1020 LSLTLRRVPKKEAHEKREHLERDLPDLPQKVVTWETVQENFLSKMEKRRDSEGEVL 1079
Db 1012 FYWVKKCFKCCCKEKNMSESSVCCFKNEDNETLAWGVKENVLYVKINTKANDT-SEEMR 1070
Qy 1080 KTAHRVDFIAKYLGG-LRQEKRIK 1103
Db 1071 HRFRLDQTKNDLKGILLKIANIK 1095

RESULT 3

US-09-636-215-778
; Sequence 778, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 778
LENGTH: 1095
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-215-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. No. 2.2e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

Qy 26 GEVNFSGSKRGKRVFVSGVAPSVLFDLLIAEHLDPANLVLSVUGEQPFAMKSWLR 85
Db 95 GDIQFETLGGK-GKYLRLSCDTEAIELLYELLTQHMLKTPNLVLSVTGAKNFALKPRMR 153

Qy 86 DVLRLKGLVKAAGTGAWILTSALRVGLARHVGQAVRDHSLASTSTKRVVAVGMASIGRV 145
Db 154 KFESR-LIIVASKGAWILTGTHGLTKYIGEVVRDNTI-SRSSEENIVAIAGWGV 211
Qy 146 LHRRILE-----EAQEDFPVHPYEDDGGSGQLCSLSDSNLSHFLIVPEFGPKGDLTELRL 202
Db 212 SNRDTLIRNCDAAGVFLAQYLMDD-FTRDPLVILDNHNNHLLVNDGCHGHPTEAKLRN 270
Qy 203 RLEKHISE---QKAGYGGTSGSIEIPVLCLLVNDGDPNLTIERISRAVQAAPWLLVCSGGI 259
Db 271 QLEKHISERTIQDSNYGG---KIPVCFAGGGKETLKAINTSIKKNPCPCVVVEGSGRI 326
Qy 260 ADVLAALVNQPHLLVPKAEKQFKEKFPK---KHFSMEDIVRWTKLQNTITSHOHLITVVD 317
Db 327 ADVIASLVEVEDAPSSAVKEKLVFLPRTVSRLESEETESIKWLKEILECSHLITVVK 386
Qy 318 FQEGSEELDTVILKALVKACKSHSQEPQDYIDELKLAIVANDRVDIAKSEIFNGDVEMKS 377
Db 387 MEEAGDEIVSNAISVALYKAFSTSEQDKDNMNGQLKLLLEWNLQDLANDIEFTNDRRWS 446
Qy 378 CDEEVMVDALYSNKPEFVRLFVNDGADVADPLTYGRLOELYRSYSRKSLLFDLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLENGLRKXFLTHDVLTELF-SNHFTSLVYRNLIQAKN 505
Qy 435 KQEEARLTLAGLGTQARPPAGPPAFSLHESVSRVLQDQACRGFYODGRPG-DRRRA 493
Db 506 SYNDALLTF-----VWKLVANFR-----RGFKEDNRGRDEMDI 539
Qy 494 EKGPAKRTGQKWLDDLNOKSNPNWRDLFLMAVLQNRHEMATYFWAMGEGVAAALAAK 553
Db 540 E-----LHDVSPITRHPQLQALFIWAILQNKLSKVIMEQTRGCTLAALGASK 587
Qy 554 ILKEMSHLETEAARAFTEA--KYERLALDLFSECYSNSEARAFALLVRRNRCWKTTC 611
Db 588 LLKTLAKVKNIDINAAGESEELANETRAVELTECYSSDEDLAEQLLYVSCBAWGSNC 647
Qy 612 LHLATEADAKAFPAHDGVOAFLTRIWWGDMAGTPTILRLGLAFLCPALVYVNLITSEEA 671
Db 648 LELAVEATDQHTAQPQGVQNFSLSKWYGEISRDITKNWKLILCFIPLVGGCFVFRKK- 706
Qy 672 PLRTGLELDQDLSLDEKSPLYGLQSRVEELVEAPRAQGRGPRAVFLLTRWRKFWGAP 731
Db 707 -----PVDKHK-----LLWYVAFFTSP 725
Qy 732 VTVFLGNVYFAFLFTVLLVDRPPPGSGPEVTLYFWVFTLVLEETROGFFTDE 791
Db 726 FVFSNWNVYFAFLFLFAVLLMDHFSVPH-----PPELVLSLVFLFCDEVRQWTVNGV 782
Qy 792 DTHLVKKFTLYVGDNNKCDMAIFLFIIVGVTCTM-----LPSAFEAGRTVLAMDVMVFTLR 848
Db 783 N-----YFTDLNWNMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLR 833
Qy 849 LTHIFAIHKQLGPKIIVVERMMKDVFFFLFSLVNLVAVGTVTQALLHPHGRLEWIFRR 908
Db 834 LTHIFTVSRNLGPKIIMQLMLIDVFFFLFSAVNVAFVARQGLRQNEQSRWIFRS 993
Qy 909 VLYRPYLOIFGOIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLYANWLVLILL 959
Db 894 VIYEPYLAIFMGQVPSD-VDGTTTDFAHCTFTGNEKPLCVELDEHNLPR-FPEWITIPIV 951
Qy 960 VTFLLVTVNLLMNLIAFMSYTFQVVGADMFVKFORVNLVIEYHERPALAPPTLLSH 1019
Db 952 CIYMLSTNILLNVLVAMFGYTVGVQENNDQVWKFQRYFLVQVYCSRLNIPFPFIVPAY 1011
Qy 1020 LSLTLRRVPKKEAHEKREHLERDLPDLPQKVVTWETVQENFLSKMEKRRDSEGEVL 1079
Db 1012 FYWVKKCFKCCCKEKNMSESSVCCFKNEDNETLAWGVKENVLYVKINTKANDT-SEEMR 1070
Qy 1080 KTAHRVDFIAKYLGG-LRQEKRIK 1103
Db 1071 HRFRLDQTKNDLKGILLKIANIK 1095

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RESULT 4
US-09-685-166A-778
; Sequence 778, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. NO. 2.2e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

QY 26 GEVNFSGGKRGKGFVRVPSGVA SVLFDLLAEWHLPAPNLVSLVGEQPFAMKSWLR 85
DB 95 GDIQETUGKR-GKIRUSCDTDAEILYELLTQHWHLTPNLVSVTGAKNFALKPRMR 153

QY 86 DVLKRGVLKAAQSTGAWITLSALRGLARHVQAVRDSLASTSTKVRVAVGMSLGRV 145
DB 154 KIFSR-LIYIAQSGAWITLGTGTHVGLTKYIGEVVRDNTI-SRSEENIVAIGIAAGWV 211

QY 146 LHRRIE---BAQEDFPVHYEDDGGSGPLCSLDSNLSHFILVEPPGPGKDGTEURL 202
DB 212 SNRDTLRNCDAEGYFLAQYLMDD--FTRDPLYLNNHNLHLLVNDNGCHGHTVTEAKLRN 270

QY 203 RLEKHIS--ORAGYGTGSIETIPVLCLLVNGDPTLIERISRAVEQAAPMLILVSGGI 259
DB 271 QLEKHISRTIQDSNYG---KIPVCFAGGKGTUKAINTSINKNIPCVVVEGSGRI 326

QY 260 ADVLAALYNQPHLLVPKVAEQKFKPPS--KHFSWEDIVRWTKLLQNTSHOHLTYVD 317
DB 327 ADVIASLVEVEDAPTSSAVKEKVRFLPRTVSRLSSEETESGWIKWKEILECSHLLTVIK 386

QY 318 PEQEGSELDIVILKALVKACKSHQEPQDVLDELKLAVDNRVDIAKSEIFENGVEWKS 377
DB 387 MEEAGDEVSNIAISYALYKAFSTSEQDKDNWNGQLKLEWNLQDLANDEIFTNDRRWES 446

QY 378 CDLEWVMVDALVSNKPEPFLVNDGADVADFLTYGRLOELYRSVSRKSLFDLLQ---R 434
DB 447 ADLQEWMTALIKDRPKFVRFLNGLNRLKFLTHDVLTELF-SNHFTLVYRNLIQAKN 505

QY 435 KOEEARLTLAGLGTQOAREPPAPFASLHVESVRVLKDFLODACGFGYODGRPG-DRRRA 493
DB 506 SYNDALLTF-----VWKLVANFR-----RGRFKEDRNGRDEMID 539

QY 494 EKGPAKRP TGQKWLDDLNKSENPNRDLFLNAVQLNRHEMATYFWAMQEGVAAALACK 553

Db 540 E-----LHDVSPITRHPLOALFIWAILQNKELSKVWEQTRGCTLAALGASK 587
QY 554 ILKEMSHLETEAEARATREA--KYERLALDLFSECYSNSEARAFALLVRNRQWSKTKC 611
Db 588 LLKTLAKKNDINAAGESEELANEYETRAVELFTECYSSDDLEAQLLVYSCWAGGSGNC 647
QY 612 LHLATEADAKAFFAHDGVQAFETIRWMDMAAGTPILRLLGAFALCPALVYTNLTJFSEA 671
Db 648 LELAVENTDQHFTAQPGVQNFSLSKQYGEISRDITKNWKIILCLFIPLVGGFGVFRKK- 706
QY 672 PLRTGLEDLQDLSLDEKSPLYGLQSRVBELEAPRAQGRGPRPAVFLLRWRKFWCAP 731
Db 707 -----EVDXHKK-----LLWYVAFETSP 725
QY 732 VTVELGNVMYFAFLFELFTYVLLVDERPPQPGSGPEVTLFWVFTLVLEIRQGFTEDE 791
Db 726 FVFSWNVVYFAFLFELFAYVLLMDFHSVPH---PPELVLSLVFVFCDEVQRQWYNGV 782
QY 792 DTHLVKKFTLYVGNWNKCDMVAIFLFIVGVTCRM---LPSAFAGRTVLAMDFWVFTLR 848
Db 783 N-----YFTDLNVMMDTGLFYFIAGIVFRLHSSNKSLSYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHKQLGPKLIIVVERNMKQVFFLPFLSVLWYAYGVTTCALLHPHGDGRLEWIER 908
Db 834 LIHIFTVSRNLGPKIIMLQRLMDVFFFLFLFAYVMVAFGARQIGILRQNEQRWRWIFRS 893
QY 909 VLYRPYLIQFGOIPLDIDEAR---VNCS-----THPLLE-DSPSCPSLVANMLVLL 959
Db 894 VIPEYLAAMFGQVPSD-VDGTTYDPAHCTFTGNESKPLCVDELDEHNLP-RPPEWITIPLV 951
QY 960 VTFLVTNVLMLNLLIAMFSYTFVQGNADMFWKFORYNLIVYHERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTVOENNQVWKFORFLVQVYCSRLNIPFPFIVPAY 1011
QY 1020 LSLTLRVFKKEAEHKEHLELDLPDLPDQVVTWETQENFLSKMEKRDRDSEGEVLR 1079
Db 1012 FYMVVKKCFKCCCKEMNESSVCCFKNEEDNETLAWGVKENVLYINKTANDT-SEMR 1070
QY 1080 KTAHRVDPIAKYLGQ-LREQEKRIK 1103
Db 1071 HRFQDLTKLNDLKGLLXKIANIK 1095

RESULT 5
US-09-636-215-780
; Sequence 780, Application US/09636215
; Patent No. 6620322
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 780
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-636-215-780

Query Match      25.6%; Score 1558.5; DB 4; Length 1095;
Best Local Similarity 34.1%; Pred. No. 1.4e-143;
Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;

QY 26 6GVNFGSGKKGKRVVPVSGVAPSLFDLLLAELHLPAPNLVSVLGVGEQPFAMKSLR 85
Db 95 GDIQFETLGGK-GKYIRLSCDTHAEILYELLTQHWHLKTPLNIVSVTGAKNFALKPMR 153
QY 86 DVLRLKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 154 KIFSR-LIVIAQSKGAWILTGTHYGLMKYIGEVVRDNTI-SRSSEENIVAIGIAAGMV 211
QY 146 LHRRIE----EAQEPFVHYPEDDGSQGPLCSLNSLHFLVBPFGPKGDGLTELRL 202
Db 212 SNRDLIRNCDAEGYFLAQLMDD-FTRDPLYLNNHTHLLVNDGCHGHTPEAKLRN 270
QY 203 RLEKHISE--ORAGYGGTSGTIEIPVCLLVNDPNTLERISRAVEQAAPMLILVSGSGI 259
Db 271 QLEKYSERTIQDSNYG---KIPVCAQGGKETLKAINTSINKKIPCVVVEGSGI 326
QY 260 ADVLAALVNQPHLLVPKVAEKOFKEKFPs--KHFSWEDIVRMTKLLQNTISHQLLTVYD 317
Db 327 ADVIASLVEVEDALTSASVAKELVPLRTPVSRSLPEETESMIKMLEKLECSHLLTVIK 386
QY 318 FPOGSEELDTILKALVACKSHSQEPDYLDELKLVAVDRVDIAKSEINFGDVEWKS 377
Db 387 MEEAGDEIVSNAISALYKAFSTSEQDKDNWNGQLKLEWNLQDLANDEIFTNDRRWES 446
QY 378 CDLEEVMDVALSNKPEFVFLVNDGADVADFLTVGRLOELYSRSRKSLLFDLLQ---R 434
Db 447 ADLQVMTFALTKDRPKFVRLLENGLNLRKELTHDVLTELF-SNHFTLVYRNQIAKN 505
QY 435 KOEERLTLAGLTQOAREPPAPAFSLHESYRVLKFLQDACRGFYQDGRPG-DRRRA 493
Db 506 SYNDALLTF-----LHDVSPITRHLQALFIAWLNQKLSKVIMEQTRGCTLAALGASK 587
QY 494 EKGPAKPTGQKWLIDLNOKSNPWRDLFLWAVLQNRHEMATYFWAMQGEVAAALAAOK 553
Db 540 E-----LHDVSPITRHLQALFIAWLNQKLSKVIMEQTRGCTLAALGASK 587
QY 554 ILKEMSHLFEAEARATREA--KYERLALDFSECYSSEARAFALLVRRNRCKSKTTC 611
Db 588 LUKTAKVNDINAGESELANEYETRAVELFETCYSDDEDLAEQLLYSCAANGSGNC 647
QY 612 LHLATEADAKAFADHGVQAFLTRIWWGDMAAGTPIRLLLGAPLCPALVYTNLITFSEBA 671
Db 648 LELAVEATDQHFIAQGVGNFLSKQWYGEISRDQTKWKKILCLFIPLVGCQGVSEPKK- 706
QY 672 PLRTGLELDQLDLSLDTESKPLVGLQSRVEELVEAPQAQDGRPAVFLTLTRWRKFWGAP 731
Db 707 -----PVDKHKK-----LLYYVAVFTSP 725
QY 732 VTVFLGNVMVYPAFLFTYVILLVDFRPPQPGSGPEVLYFWVFTLVLEIEIRQGFETDE 791
Db 726 FVVFSSNVVYFAFLFLYVLLMDFHSVPH---PPELVLYSLVFLVFCDEVRQWTVNGV 782
QY 792 DTHLVKKFTLYVGDNNWKNCDMAIFLIVGVTCRM---LPSAFEAGRTVLAQDMFVFTLR 848
Db 783 N-----YPTDLNWNVDTLGLFFYIAGIVFRLHSSNKSLSYGRVIFCLDYIIFTLR 833
QY 849 LHIHFAIHKQLGPKIIVVERMMKDVFFLFFLSVWLVAVGVTTQALLHPHDGRLEWIFRR 908
Db 834 LIHIFTVSRNLGPKIIMLQRMILIDVFLLFLFAXWNVAFVQFQILRQNEQRWRWIFRS 893
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QY 909 VLYRPLYQIFQIPLDEIDEAR---VNCS-----THPLLE--DSPSCPSLYANWLIVLL 959
Db 894 VIYEPYLAQFQVPSD-VGDTTYDFAHCTFTGNSKPLCVELDEHNLPR-FPEWITIFLV 951
QY 960 VTFLLVNTVLLMNLIAFPSYTFQVQGNADPMFKQRYNLIVYHERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTVGQENNDQVWKQFQRYFLVQVYCSRLNIPFPFIVPAY 1011
QY 1020 LSLTIRRYPKKEAEHREHLERDLDPDLQKVVVTVETVOKENFLSKMEKRRDSEGEVLR 1079
Db 1012 FYMVYKCKFCCKCKKNMSESSVCCFKNEDNETLAWGVMKENLYKINTKANDT-SEMR 1070
QY 1080 KTAHRVDFTIAKYLGG-LREQEKRIK 1103
Db 1071 HRFRQDITKINDLKGLLKEIANKIK 1095
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RESULT 6

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US-09-685-166A-780
; Sequence 780, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-685-166A-780
```

```
Query Match      25.6%; Score 1558.5; DB 4; Length 1095;
Best Local Similarity 34.1%; Pred. No. 1.4e-143;
Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;

QY 26 6GVNFGSGKKGKRVVPVSGVAPSLFDLLLAELHLPAPNLVSVLGVGEQPFAMKSLR 85
Db 95 GDIQFETLGGK-GKYIRLSCDTHAEILYELLTQHWHLKTPLNIVSVTGAKNFALKPMR 153
QY 86 DVLRLKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 154 KIFSR-LIVIAQSKGAWILTGTHYGLMKYIGEVVRDNTI-SRSSEENIVAIGIAAGMV 211
QY 146 LHRRIE----EAQEPFVHYPEDDGSQGPLCSLNSLHFLVBPFGPKGDGLTELRL 202
Db 212 SNRDLIRNCDAEGYFLAQLMDD-FTRDPLYLNNHTHLLVNDGCHGHTPEAKLRN 270
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Qy	203	RLEKXISE---ORAGYGGTGSIBIPVCLLVGNPDNTLERTSRAVEQOAPMWLLVSGSGI	259
Db	271	QLEXYISERTITQDSNYGG---KTIPIVFAQGGGKETLKATINTSIKKNIPCVWVEGSGOI	326
Qy	260	ADVLAALVNQPHLLVPKVAEQKFEKPPS--KHFSWEDIVMTWTKLQWITSHQHLITVYD	317
Db	327	ADVTASLVVEVDALTSSAVKGLVRFLPRTVSRLPPEETESWIKWKEILCESHLITVIK	386
Qy	318	PEQEGSEELDTVIILKALVKACKSHSQEPQDLDLKLAVADRVDIAKSEIFNGDVIEWS	377
Db	387	MEEAGDEIVSNAISVALYKAFSTEQDQDNWNGQLLLENNQLDLANDEIFTNDRRWES	446
Qy	378	CDLEBVMVDALVSNKPBEVRULPVNDGADVADFLTYGRLOELYRSVRSKSLFLDQLQ---	434
Db	447	ADLOEVMFTALIKDRPKFVRFLFLENGLRFLKRLFDHVLTELF-SNHFSFTLYVRNLQIAKN	505
Qy	435	KQBEARLTLAGIGTCQAREPPAGPAPFASLHEVSRVLQDQACRGFFQDCRPG--DRRA	493
Db	506	SYNDALLTF-----VWKLVANFR-----RGFRKEDRNGRDEMDI	539
Qy	494	EKGPAKRPTGOKWLLDLNOKSENPRDILFLWAVLQNRHEMATIYFWMQOEGVAAALAAACK	553
Db	540	E-----LHDVSPITRHPQLQALFIWAILQNKKELSKVITQEGRGCTTLAALGASK	587
Qy	554	ILKEMSHLETAEBARAATREA--KYERIALDLFSHCYSNSRARAPALLVRNRCSWKTC	611
Db	588	LLKTLAKKNDINAGASEELANEYETRAVELFTCYCSDSDLABQLLVYSCAEMGGSGNC	647
Qy	612	LHLATEADAKAFFAHDGVQAFLTRIWMGDMAAGPTILRLIAGFLCPALVYTNLITFSEA	671
Db	648	LELAEATDQHFTIAPQGVNFSKOWYGEISRDTKWKKIILCLFTIPLVGGCGFSFRKK-	706
Qy	672	PLRTGLEDLQDLSDLTEKSPLYGLIQSRVEELVEAPRAQGRGPRAPVLLTRWRKFWGAP	731
Db	707	-----PVDRKHK-----LLWVYVAFVTFSP	725
Qy	732	VTVPFGNVVMYFAFLFTYTVLLVDPRPPQPGSPGPEVTLVFWVFTLWLEIRQGFTHDE	791
Db	726	FWFVSNWVYFIAFULLPAYVLLMDFHSGVPH---PPELVLYSLVPVLCDFCEVRQWYNGV	782
Qy	792	DTHLVKFFTLVGVGNWKKDMVAFLFTVGVTCRM--LPSAFAGRVTLAMDPMVFTLR	848
Db	783	N-----YFTDLNWNMDITGLFYFTAGIVFRLHSSNKSLSYSGRVICLDYIIFTLR	833
Qy	849	LIHIFAHKQGLGPKIIVVERMMKDVFFLFFLSVWLVAYGVTTQALLPHDGRLEWIFRR	908
Db	834	LIHIFTVSRNLGPKIIMLQMLDVFVFFLELFAKMWAFVARQGLAQNEQRWEIERS	893
Qy	909	VLYRPIQIFQOILDEIDEAR---VNGS-----THPLLLE--DPSPCSLVYANLVULL	959
Db	894	VIVPEYLAAMFQGVPSD-VDGTITYDPAHCTFTGNESKPLCVELDEHNLRP-FPEWITIPLV	951
Qy	960	VTFLVTVNLVLLMILLIAMFSYTFQVQGNADMFWKFORYNLIVYHERPALAPPILLASH	1015
Db	952	CYIMLSNRNILLVNLVAMFGYTVGVQENNDQVWKFQRYFLVQEYCSRLNIPFPFIVFAY	1015
Qy	1020	LSLTLRLVRKKEAEHKBHLERDLPDLDQKVVWTWETVQENFLSKMEKRRDRSSEVLRL	1075
Db	1012	FYMWVKCFCKCKCEKNWESSVCCFKNEDNETLAWGVKENVLYKINTKANDT-SEWR	1075
Qy	1080	KTAHRVDFIAKVLGG-LREQEKRIK	1103
Db	1071	HRFQGLDTKLNDLKGLLKEIANKIK	1095

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RESULT 7
US-08-623-679-9
; Sequence 9, Application US/08623679
; Patent No. 5674739
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR
;

```

```
; TITLE OF INVENTION: PROGRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,679
; FILING DATE: 29-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,431
; FILING DATE: 29-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1533 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-623-679-9

Query Match      20.4%; Score 1240.5; DB 1; Length 1533;
Best Local Similarity 28.0%; Pred.No.5.3e-112;
Matches 357; Conservative 230; Mismatches 449; Indels 241; Gaps 38;

QY    40   EVRVSGVAPSVLFDLLLAEBWHLPAPNLVSLVGEEPPFAKMSWLRDVLRLKGVLKAAQST 99
Db    2   YIRVSVDTKPDSLHLHMKWDQLLEPKLLISVIGGLQNFEMQPXLKVQFGKGLIKAAATT 61

QY    100  GAMILTSALRVLGHVQAARDHSLASTSTKYRVAVAGMASGRVLHRRILEEAQEDF - 158
Db    62   GAMIFTGGVGTGVISHVGDALKDH---SSKSGRVCAGIAPGIV-----ENKEDLV 111

QY    159   ---PVHPEDDGSGQGPLCSLDNSLHSHPIUVEPGPGKGDGLETLRLRLKHISEQ---- 211
Db    112  GKDVTRYVTQMSNPLSKLSVINNSHTFIADNGTGLGYGAEVKLRLLEKHSLOKINT 171

QY    212  RAGVGGNGSIEIPVICLVNGDNTLERISKAVEQAAPWLILV--GSGGIADVLA----- 264
Db    172  RLQQG-----VPLVLGVVEGGNVVISVILEYLOEPPPVPVIICDSSGRASDILSAHKY 225

QY    265   ----ALVNO---PHLLVPKVAEKQFKBKFPSPHSWEDIVRWTKLQNITSHOHLTVYD 317
Db    226  CEEGGIINESLREQLLV--TIQKTENVYNAQSHQFALIMECKM-----KKELVTVFR 276

QY    318  FEQGSBELTVILKALVKACKSHSQBPQDYLBELKLAVAWDRVDIAKSEIFNGDVEW-- 375
Db    277  MGSEGQQDIEMAILTALLKG--TNVSAP-----DQLSLAANWRVDIARSQIFVFPGHWTP 330

QY    376   -----KSCD----- 379
Db    331  LGSILAPPTDSKAITEKEKKPPMATTKGGRGKGGKKGKVKVEEVEETDPKRIELLNWNA 390

QY    380  LEVMVDALVSNKPFEFVLRFVNDGNAVDFITYGRLOELYRSYSRKSLFLDLQRQEBA 439
Db    391  LEQAMLDALVLDVRDFVKLLLIENGNNQHFLTTPRLEELENTRILGPENTLHLLEAVRDVKS 450
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QY 440 RUTLAGLGTQQAAREPPAGPPAF--SLHEVSRVLKDFLODQACR-----GFYQD 484
Db 451 NL-----PPDVHISLIDGLVLELGMGAYRCNYTRKNFRTLYNNLFGP 494
QY 485 GRP-----GDRRAEKGPAKPTGQKWLLDLN-----QKSENPRDLFLWAVLQNR 530
Db 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEEDIDVDDPAVSRFOYPPHELVAVLWVLMKR 554
QY 531 HEMATYFWAMGOEGVAAALAAACKILKEMGHLETEABEA-----RATREAKYERLALDLF 584
Db 555 QKMAVFLAQGEESMAKALVACKLYKAMAHESSESIDLVDISQDLNNSKDFGQALALELL 614
QY 585 SECYSNSEARAFALLVRRNRCSKTTCLHLATEADAKAFPAHDGVQAFTRIWMG--DMA 642
Db 615 DOSYKHDEQIAKMLTYELKWSNSTCLKLAVAAKHRDFAHTCSQMLLTDMMGLRLMR 674
QY 643 AGTPILRLLAGLPCALVYTNLITFSEAPLRTGLEDLQDLSLDTKESPLYLGLQSRVEE 702
Db 675 KNPGLKVMINGILLPPTILFLEFRY-----DDFSYQTSKENEDEGKEEEN 720
QY 703 L---VEAPRAQGD-----RGPRAVFLLTRWRKFWGAPVTVFLGNVVMYFAFLFETYVLL 754
Db 721 TDANADAGSRKGEENEHKKQORSIPGTKICEFNAPIVKFWFYTISYLGYLLEFFNYVIL 780
QY 755 VDFRPPPGSGPEVTLYFWVFTLVLEIRQGFDTDETHLVKKFTLYYVDNWKCDMVA 814
Db 781 VRM---DGWPSLQEWIVISYIVSLALEKIRE--ILMSEPGKLSQKIKVWLQEWYNTIDLVA 836
QY 815 IFLFIVGVTCTMLPSAFEAF--GRTVLAMDPMVFTLRILHIFAIHKLQKGPKIIVVERMKDV 873
Db 837 ISTFMIGAILRLQONQYMGYGRVIYCVDIIFWIRVLDIFGVNKYLGYPVMIGMKMIDM 896
QY 874 FFELFSLVLMVAIGVTTQALLHPHDRLW--IFRRVLRYRPLYQIFGOIPLDEIDEARVN 932
Db 897 LYFVVMVLVMSFGVARQAILHPBE--KPSWKLARNIFTWYPMYIYGEVFAQID----- 950
QY 933 CSHPLLLLEDSPC-----PSLYANWLVLVLLVTLVTLVTLVTLVTLVTLVTLVTLV 979
Db 951 ----LYAMEINPPCGENLDEEGKRLPPCIPGAWLTPLMACVLLVANILLVNLVLAIVEN 1006
QY 980 YTFQVQGNADMFVKFORNLVVEHERPALAPPFTILLSLSLTLRRV---PKKEAEHXR 1036
Db 1007 NTFFEVKISNQVKFORQVQLMTFHDRVLPVPPPMIILSHIYIIINRLSGRCRKREGDQ 1066
QY 1037 EHLERDL-----PDPLDQKVTWETQKENFLSKMEKRRRDEGEVLRKTAHRVDIFAKY 1091
Db 1067 EERDRGLKFLSDEELKRLHEEEQCVQEHFPEK--EDEQSSSDEIRVTSERVENMSNR 1125
QY 1092 LGLLEQEK-----RIKLESQINYCSVLSSVADV---LAQGGPRSSQHC 1136
Db 1126 LBEINERETFMKTSLSQTVDLRLAQLAELSNRMVNALENLAGIDRSDLIQARS--RASSEC- 1183
QY 1137 EGSQVAADHRGGLDQW 1153
Db 1184 EATYLLROSSINSADGY 1200

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RESULT 8

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US-08-933-774-9
; Sequence 9, Application US/08933774A
; Patent No. 6025137
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
; FILE REFERENCE: 07334/004003
; CURRENT APPLICATION NUMBER: US/08/933,774A
; CURRENT FILING DATE: 1997-09-19
; EARLIER APPLICATION NUMBER: US 08/623,679
; EARLIER FILING DATE: 1996-03-29
; EARLIER APPLICATION NUMBER: US 08/412,431
; EARLIER FILING DATE: 1995-03-29
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-933-774-9

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Query Match      20.4%; Score 1240.5; DB 3; Length 1533;
Best Local Similarity 28.0%; Pred.No.5.3e-112; Indels 241; Gaps 38;
Matches 357; Conservative 230; Mismatches 449;
QY 40 FVRPSGVAPSVLFDLLAEWHLPAPNLVSVLVGEEQPFAMKSWLRDLVLRKGLVKAQST 99
Db 2 YIRVSYDTKPDLSLLHLMVKDWQLPLKLLSVHGGI-QNFEMQPKLQKQVFGKGLIKAAMTT 61
QY 100 GAWILTSALRVLGRHVGQAVRDHSLASTSTKRVVAVGMAISLGRVLRHRIIEAEDF- 158
Db 62 GAWIFTGVSTGVISHVGDAKDH---SSKSRVCAIGIAPWGIV-----ENKEDLV 111
QY 159 ---PVHYPEDDGGSCQPLCSLDSNLSHFTLVBPGPGKGDGLTELRLEKHLSE- 211
Db 112 GKDVTRVYQTMGNPLSKLSVLNNSHTHFLAONGTLGKYGAEVKLRRLLEKHISLOKINT 171
QY 212 RAGYGTGSIPIPLCLLVNGDENTLERISRAVEQAAPWLILV--GSGGIADVLA----- 264
Db 172 RLQGG-----VPLGLVVEGGPNVSVIVLEVLQEEPPPIPVVICGSGRASDILSFAHY 225
QY 265 ----ALVNO---PHLLVPKVAEKQKEKPPSKHFSWEDIVRWTKLLQNTSHQHLTVYD 317
Db 226 CEEGGIINESLREQLLV--TIQKTFYNKAQSHQLFAIIMECMK-----KKELVTVFR 276
QY 318 FEQEGSEELDTVILKALVKACKSHSCPEODYLDLKLAVADRDVIAKSEIFENGDVEM-- 375
Db 277 MGSEGOQDIEMAILTALLKG--TNVSAP---DQLSALAWNRVDIARSQIFVFGPHWTP 330
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QY 380 LEEVMDALVSNKPFVRFLFVNDGADVADFLTYGBLOELYRVSRSKSLFDLLQKQERA 439
Db 391 LEQAMLDALVDRVDFVLLIENGVMQHFILPIRLEELYNTRLGPPTLHLLVRDVKKS 450
QY 440 RUTLAGLGTQQAAREPPAGPPAF--SLHEVSRVLKDFLODQACR-----GFYQD 484
Db 451 NL-----PPDVHISLIDGLVLELGMGAYRCNYTRKNFRTLYNNLFGP 494
QY 485 GRP-----GDRRAEKGPAKPTGQKWLLDLN-----QKSENPRDLFLWAVLQNR 530
Db 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEEDIDVDDPAVSRFOYPPHELVAVLWVLMKR 554
QY 531 HEMATYFWAMGOEGVAAALAAACKILKEMSHLETEABEA-----RATREAKYERLALDLF 584
Db 555 QKMAVFLAQGEESMAKALVACKLYKAMAHESSESIDLVDISQDLNNSKDFGQALALELL 614
QY 585 SECYSNSEARAFALLVRRNRCSKTTCLHLATEADAKAFPAHDGVQAFTRIWMG--DMA 642
Db 615 DOSYKHDEQIAKMLTYELKWSNSTCLKLAVAAKHRDFAHTCSQMLLTDMMGLRLMR 674
QY 643 AGTPILRLLAGLPCALVYTNLITFSEAPLRTGLEDLQDLSLDTKESPLYLGLQSRVEE 702
Db 675 KNPGLKVMINGILLPPTILFLEFRY-----DDFSYQTSKENEDEGKEEEN 720
QY 703 L---VEAPRAQGD-----RGPRAVFLLTRWRKFWGAPVTVFLGNVVMYFAFLFETYVLL 754
Db 721 TDANADAGSRKGEENEHKKQORSIPGTKICEFNAPIVKFWFYTISYLGYLLEFFNYVIL 780
QY 755 VDFRPPPGSGPEVTLYFWVFTLVLEIRQGFDTDETHLVKKFTLYYVDNWKCDMVA 814
Db 781 VRM---DGWPSLQEWIVISYIVSLALEKIRE--ILMSEPGKLSQKIKVWLQEWYNTIDLVA 836
QY 815 IFLFIVGVTCTMLPSAFEAF--GRTVLAMDPMVFTLRILHIFAIHKLQKGPKIIVVERMKDV 873

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Db 837 ISTFMIGAILRLQNPYMGYGRVYICVDIIFWYIRVLDIFGVNKKYLGYYMMIGKMMIDM 896
 Qy 874 FFELFFLSVLMVAVGVTQTALLPHDGRLEW-IFRRVLYRPLYQIFGOIPLDEIDEARVN 932
 Db 897 LYFVVMVLMVMSFGVARQAILHPEE-KPSWKALRNIFYMFMWYIYGEVFADQID----- 950
 Qy 933 CSTHPLLEDSPSC-----PSLYANMLVILLVTFLLVTNVLMLNLIAMFS 979
 Db 951 ----LYAMEINPPCGENLYDBEGKRLPPCIPGAWLTPALMACYLLVANILLVNLIIAVFN 1006
 Qy 980 YTFQVQGNADMFWKFORYNLIVYHERPALAPPFILLSHLSLTLRV---FKKEAEHR 1036
 Db 1007 NTFPEVKSINQVWKFQYQIMTFHDPVLPVPPMIIISHYIIIMRLSGCRKREGDQ 1066
 Qy 1037 EHLERDL-----PDLQKVVTWETVOKENFLSKWEKRRDRSEGEVLKTAHRYDEIAKY 1091
 Db 1067 EERDGLKFLSDEELKRLHEFEQCQVEHPEK-EDBQSSSDEIRVTSERVENMSMR 1125
 Qy 1092 LGGUREQEK-----RIKLESQINYCSVLVSSVADV---LAQGGGPRSSQHCQ 1136
 Db 1126 LEEINERETFMKTSIQTVDLRLAQLLELSNRMVNALENLAGIDRSDLIQARS-RASSEC- 1183
 Qy 1137 EGSOLVAADHRGGLDGM 1153
 Db 1184 EATYLLROSSINSADGY 1200

RESULT 9

US-09-181-030-9
 ; Sequence 9, Application US/09181030
 ; Patent No. 6251597
 ; GENERAL INFORMATION:
 ; APPLICANT: Shvlian, Andrew W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
 ; TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
 ; FILE REFERENCE: 07334/004005
 ; CURRENT APPLICATION NUMBER: US/09/181,030
 ; CURRENT FILING DATE: 1998-10-27
 ; EARLIER APPLICATION NUMBER: US 08/862,442
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: US 08/623,679
 ; EARLIER FILING DATE: 1996-03-29
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 1533
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-181-030-9

Query Match 20.4%; Score 1240.5; DB 3; Length 1533;
 Best Local Similarity 28.0%; Pred. No. 5,3e-112;
 Matches 357; Conservative 230; Mismatches 449; Indels 241; Gaps 38;
 Qy 40 FVRVSGVAPSVLFDLLAEWHLPAIPLVSVLSVGEQPPAKMSWIRVLRKGLVKAOST 99
 Db 2 YIRVSYDKPSSLLHLMVKDQWOLELPKLLISVHGQLQNFEMQPKLQVFGKGLIKAAATT 61
 Qy 100 GAWILTSALRYGLABHVGOVDPDHSLASTSTKVRVYVGMASIGSLVHLRHLLEEAQEDF- 158
 Db 62 GAWIFTGVSTGVISHVGDALKDH---SKSRGRVCAIGIAPWGIV-----ENKEDIV 111
 Qy 159 ---PVHYPPDDGSGQPLCSLDNLSHFLVLPBPGPGKDGITELRLRLKHXISBQ----- 211
 Db 112 GKDVTRVYQTMENPLSKLSVNNSTHTFLADNGTLGKYGAEVKLRLLRLLKHXISLQKINT 171
 Qy 212 RAGYGGTGSIEIPVLCILVNGDPNPTLERISRAVEQAAPWLILV---GSGGIADVLA----- 264
 Db 172 RLQGC-----VPLVGLVVEGGPNVSVIYLEIQEPEPTPVVICDGSGRASDILSFAHKY 225
 Qy 265 ----ALVNO---PHLLVPKVAEQKPEKPPSKHPSWEDIVRTWTKLQNTSHOHLITVDY 317
 Db 226 CEEGIIINESLREQLLV---TIQTFNFKYKAQSHQLFAIMECK-----KKELVTYFR 276

Qy 318 FEQGSBELDTVLKALVKACKSHSQBPQDYLDLDELKLAVADWVDVIAKSIFFNGDVBW-- 375
 Db 277 MGSEGGQDIEMAILTALLKG--TNVSAP-----DQLSLAANWRVDIARSOIFVPGHPWP 330
 Qy 376 -----KSCD----- 379
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 Qy 485 GRP-----GDRRAEKGPAPKPTQCKWLLDLN-----OKSENWRDLFLWAVLQNR 530
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 Qy 585 SECYSNSEARAFALLVRRNRCWKTCTCLHLATEADAKAFAHGDVQVQAFLTRIWWG--DMA 642
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 Db 781 VRM---DGWPSLQEWIVISYIVSLALEKIRE-ILMSPGKLSQKIKVWLQEQYMNITDVA 836
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 Db 897 LYFVVMVLMVMSFGVARQAILHPEE-KPSWKALRNIFYMFMWYIYGEVFADQID----- 950
 Qy 933 CSTHPLLEDSPSC-----PSLYANMLVILLVTFLLVTNVLMLNLIAMFS 979
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 Qy 980 YTFQVQGNADMFWKFORYNLIVYHERPALAPPFILLSHLSLTLRV---FKKEAEHR 1036
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 Qy 1037 EHLERDL-----PDLQKVVTWETVOKENFLSKWEKRRDRSEGEVLKTAHRYDEIAKY 1091
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 Qy 1092 LGGUREQEK-----RIKLESQINYCSVLVSSVADV---LAQGGGPRSSQHCQ 1136
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 Qy 1137 EGSOLVAADHRGGLDGM 1153
 Db 1184 EATYLLROSSINSADGY 1200

RESULT 10

US-09-534-242-9
 ; Sequence 9, Application US/09534242

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485	Qy	485	GRP-----GRRRAEKGPARKPTGQKWLDDLN-----QKSENPMWDLFWAVLQNR	530
495	Db	495	KRPKALLGWEDDEPPAKGKKKKKKKEEIDIDVDDPAVSRFQYFPHLMVWVLMKR	554
531	Qy	531	HEMATYFWANQCEGVAALAAACKILKEMSHLETEAEAA-----RATREAKYERLALDLF	584
555	Db	555	OKMAVFLWQGBESMAKALVACKLYKAMAHESSESDLVDDISQOLDNNSKDFGQALAE LL	614
585	Qy	585	SECVSNEARAFALLVRRNRCSKTTTCLHLATEADAKAFPAHDGVQAFLTRIWMG--DMA	642
615	Db	615	DQSYKHDEQIATKMLTVELKNWSNSTCLKVAAKHRDFIAHTCSQMLLTDMMWGRUMR	674
643	Qy	643	AGTPILRLLAGFLCAPLVYTNLITFSEAPLRTGLEDLQOLDLSDLTSEKSPLYGLQSRVEE	702
675	Db	675	KNPGLKVMIGILLPPTILFLFERTY-----DDFSYQTSKENEDGKEEEN	720
703	Qy	703	L---VEAPRQGD-----RGPRAVELLTRRKFWGAPVTVPLGNVVMYFAFLFTVVL	754
721	Db	721	TDANADAGSKGBEENBHKQSRIPGTKECFYNAPIVKFWFTTISYLGYLLENFNVIL	780
755	Qy	755	VDFRPPQSGSGBEVTLFYFWVFTLVLEBEIRQGFPTDEDTHLVKFTLYLVGDNWKNCDMVA	814
781	Db	781	VRM---DGWESLQEWIVISIVSLAEKIRE-IIMSEPGKLSQIKVWLOEYWNITDLVA	836
815	Qy	815	IFUFIUGVTCRMLPSAFEA-GRTVLAMDPMVFTLRLIHI FAHKQLGPKIIVVERMMKDV	873
837	Db	837	ISTFMIGAILRLQNPQMGYGRVTCVDITFIWYIRVLDFGVNKYLGFYVMMIGKWMIDM	896
874	Qy	874	FFELFSLVWLAVGVTTOALLHPHGRLEW-IFRRVLYRPYLOIFQOIPLDEIDEARVN	932
897	Db	897	LYFVIMLVMLSPGVARQAILHPEE-KPSWKCLARNIFYPMWMIYGEVADQID-----	950
933	Qy	933	CSTHPLLEDSPSC-----PSLYANMLVILLVTLVTLVTVNVLNMLLIAMFS	979
951	Db	951	----LYAMEINPPCGENLYDBEGKRLPCTPGAWLTALMACYLLVANILLVLLIIVFN	1006
980	Qy	980	YTVQVQGNADMFVKORYNLIVVEYHERPALAPPFILLSHLSLTLRRV---FKPEAEHRK	1036
1007	Db	1007	NTTFEVKSIQNQWKFQRYQLIMTFHDRPVLPPPMIILSHIYIIMLSGRCKRKREGDQ	1066
1037	Qy	1037	EHLERDI-----PDPLDQKVVTWETQKENFLSKWEXERRDSEGEVLRKTAHRVDFTAKY	1091
1067	Db	1067	EENDRGUKFLSDEELKRLHEFEQCVOEHFREK-EDEQOSSSDERIRVTSERVENMSMR	1125
1092	Qy	1092	LGLIREQEK-----RIKLESQINYCSVLVSSVADV----LAQGGGPRSSOHCQ	1136
1126	Db	1126	LEEINERETFMKTSLOTVDLRLAQLLELSNRMVNALENLAGIDRSDLIQARS-PASSEC-	1183
1137	Qy	1137	EGSOLVAADHRGGLDGW	1153
1184	Db	1184	EATYLLRFQSSINSADGY	1200

RESULT 13

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US-08-623-679-7
; Sequence 7, Application US/08623679
; Patent No. 5674739
; GENERAL INFORMATION:
; APPLICANT: Shvjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR
; TITLE OF INVENTION: PROGRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

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is Page Blank (uspto)

Brannock
10/02/2018
Seq ID 8

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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:00:43 ; Search time 73 Seconds
(without alignments)
4509.149 Million cell updates/sec

Title: US-10-026-188-8
Perfect score: 6093
Sequence: 1 MQDVQGRPGSPGDAEDRRE.....HRGGLDGEQPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6093	100.0	1165	5	ABB83855	ABB83855 Human ltr
4	6034	99.0	1179	4	AAB86165	AAB86165 Human MTR
5	5088.5	83.5	1158	4	AAB86164	AAB86164 Mouse MTR
6	5088.5	83.5	1158	5	ABB83854	ABB83854 Mouse ltr
7	5080.5	83.4	1158	4	AAB86166	AAB86166 Mouse MTR
8	5073	83.3	1157	5	AAM51707	AAM51707 Mouse TRP
9	5008.5	82.2	1164	5	ABB83853	ABB83853 Rat L-TRP
10	4534	74.4	872	4	AAB86163	AAB86163 Human MTR
11	2448.5	40.2	1166	5	ABG61907	ABG61907 Prostate
12	2448.5	40.2	1214	3	AAY95436	AAY95436 Human cal
13	2448.5	40.1	1214	5	AAE20283	AAE20283 Human TRP
14	2412.5	39.6	1129	4	AAB85974	AAB85974 Human T1C
15	2353	38.6	1083	6	ABG72088	ABG72088 Human tra
16	2184.5	35.9	1040	5	AAB82018	AAB82018 Human sec
17	2164	35.5	1016	5	ABG61852	ABG61852 Prostate
18	2039	33.5	1469	6	ABR43185	ABR43185 Human REM
19	2039	33.5	1503	3	AAY92944	AAY92944 Human TRP
20	2039	33.5	1503	3	AAY95439	AAY95439 Human cal
21	2039	33.5	1503	3	AAB36865	AAB36865 Human put
22	2039	33.5	1503	5	ABB76459	ABB76459 Human lon
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31	1574.5	25.8	1104	3	AAY95437	AAY95437 Human cal
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33	1566.5	25.7	1095	4	AAM01233	AAM01233 P788P ani
34	1566.5	25.7	1095	4	AAB69878	AAB69878 Human pro
35	1566.5	25.7	1095	4	ABU71769	ABU71769 Prostate
36	1566.5	25.7	1095	5	ABB95338	ABB95338 Human P78
37	1566.5	25.7	1095	6	ABR54450	ABR54450 Prostate
38	1566.5	25.7	1095	7	ADB75597	ADB75597 Prostate
39	1566.5	25.7	1095	7	ADB75597	ADB75597 Prostate
40	1563.5	25.7	1104	5	ADB14228	ADB14228 Human pro
41	1558.5	25.6	1095	4	ABG61818	ABG61818 Prostate
42	1558.5	25.6	1095	4	AAM01234	AAM01234 P788P ani
43	1558.5	25.6	1095	4	AAB69879	AAB69879 Human pro
44	1558.5	25.6	1095	5	ABB95339	ABB95339 Human P78
45	1558.5	25.6	1095	6	ABR54451	ABR54451 Prostate

ALIGNMENTS

RESULT 1

AAB86162
ID AAB86162 standard; protein; 1165 AA.

AC AAB86162;

DT 09-AUG-2001 (first entry)

DE Human MTR1 protein containing exon 18 fragment.

MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
intracellular calcium ion regulation; hormone; growth factor; apoptosis;
cell growth; cell death; cell differentiation; urogenital disease;
polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
rhabdomyosarcoma.

OS Homo sapiens.

FN WO200132693-A2.

XX 10-MAY-2001.

PF 06-NOV-2000; 2000WO-DE003876.

PR 04-NOV-1999; 99DE-01053167.

PA (UYGU-) UNIV GUTENBERG JOHANNES.

PI Prawitt D, Pelletier J, Zabel B;

DR WPI, 2001-316417/33.

DR N-ESDB; AAH20574.

PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann

PS syndrome and tumors, also related proteins and antibodies.

CC Claim 10; Fig 4; 46pp; German.

CC This invention describes a novel DNA sequence (I) encoding the MTR1
protein that: (i) has at least one biological activity of a TRP
protein; (ii) is connected with
etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
with tumors involving 11p15.5 abnormalities. The products of the
invention have anticancer and developmental activity. MTR1 is involved in
regulation of intracellular calcium ion levels, which are essential for
cellular responses to hormones and/or growth factors; also in apoptosis

CC and cell growth, death and differentiation, and in urogenital diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases
 CC associated with altered expression of the MTR1 gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
 CC thalidomide tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers, for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers, for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents a human MTR1 protein described in the method of the invention
 XX

SQ Sequence 1165 AA;

Query Match 100.0%; Score 6093; DB 4; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQDVQGRPGSGDAERELGLHGEVNFVGGSGKKGKGFVRVPSGVAPSVLFEDLLAEW 60
 DB 1 MQDVQGRPGSGDAERELGLHGEVNFVGGSGKKGKGFVRVPSGVAPSVLFEDLLAEW 60

QY 61 HLPAPNLVSVLNGEEQPFAMKSLRDVLRKGLVKAAGSTGAWILTSALRVGLARHVQAV 120
 DB 61 HLPAPNLVSVLNGEEQPFAMKSLRDVLRKGLVKAAGSTGAWILTSALRVGLARHVQAV 120

QY 121 RDSLSASTSKRVAVGMSLGRVLRHRRILEEAQEDFPVHYPEDDGGSGQPLCSLDSNL 180
 DB 121 RDSLSASTSKRVAVGMSLGRVLRHRRILEEAQEDFPVHYPEDDGGSGQPLCSLDSNL 180

QY 181 SHFLVPEPGKGDGLTELRLEKHI SEORAGYGGTSGIEIPIVCLLVNGDPTLIERI 240
 DB 181 SHFLVPEPGKGDGLTELRLEKHI SEORAGYGGTSGIEIPIVCLLVNGDPTLIERI 240

QY 241 SRAVEQAAPWLLVVGSGGIADVLALVNQPHLLVPKVAEQKFKEKFPKHSWEDIVRWT 300
 DB 241 SRAVEQAAPWLLVVGSGGIADVLALVNQPHLLVPKVAEQKFKEKFPKHSWEDIVRWT 300

QY 301 KLLQNTITSHQHLTVYDFEQQSGBELDTVILKALVKAACKSHSQBPQDYLDLKLAVAWDR 360
 DB 301 KLLQNTITSHQHLTVYDFEQQSGBELDTVILKALVKAACKSHSQBPQDYLDLKLAVAWDR 360

QY 361 VDIAKSIFNGDVEMKSCDLEEVMDVLSNKPFEVRLFDVNGADVADFLTYGRLQELYR 420
 DB 361 VDIAKSIFNGDVEMKSCDLEEVMDVLSNKPFEVRLFDVNGADVADFLTYGRLQELYR 420

QY 421 SVSRKSLFLDLQKQBEARLTLAGLTQQAAREPPAGPAPFSLHEVSRVLDKDFLQDACRG 480
 DB 421 SVSRKSLFLDLQKQBEARLTLAGLTQQAAREPPAGPAPFSLHEVSRVLDKDFLQDACRG 480

QY 481 FYQGRPGDRRAEKPAKRTQKWLIDLNQKSENPRWDLFLWAVLQNRHEMATYFWAM 540
 DB 481 FYQGRPGDRRAEKPAKRTQKWLIDLNQKSENPRWDLFLWAVLQNRHEMATYFWAM 540

QY 541 GQGVAAALAAKCKILKEMSHLETAEARATREAKYERLADLSECVSNSEARAFALLV 600
 DB 541 GQGVAAALAAKCKILKEMSHLETAEARATREAKYERLADLSECVSNSEARAFALLV 600

QY 601 RRNRCSWKTTCCLHATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLIGAFCLPALV 660
 DB 601 RRNRCSWKTTCCLHATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLIGAFCLPALV 660

QY 661 YTNLITSEAPLRTGLDLQDLSLDEKSPILGLQSRVLELVEAPRAQDGRGPRAVFL 720
 DB 661 YTNLITSEAPLRTGLDLQDLSLDEKSPILGLQSRVLELVEAPRAQDGRGPRAVFL 720

QY 721 LTRWRKFWGAPVTYFLGNVMVYAFLEFLFTTVLLVDFRPPQPGSPPEVTLYFWVFTLV 780
 DB 721 LTRWRKFWGAPVTYFLGNVMVYAFLEFLFTTVLLVDFRPPQPGSPPEVTLYFWVFTLV 780

QY 781 EETROGFFTDDETHLVKFTLYVGDNNWKNCDMVAIFLVGVTCRMLPSAFEAGRTVLAM 840
 DB 781 EETROGFFTDDETHLVKFTLYVGDNNWKNCDMVAIFLVGVTCRMLPSAFEAGRTVLAM 840

QY 841 DMVFTLRLLIHFPAIHKQLGPKLIIVVERMKDVFFLFFLSVWLVAVGVTTOALLHPHDG 900
 DB 841 DMVFTLRLLIHFPAIHKQLGPKLIIVVERMKDVFFLFFLSVWLVAVGVTTOALLHPHDG 900

QY 901 RLSEWIFRRVLYRPLYQIFGOIPLDEIDEARVNCSTHPLLEDSPSCSLYANMLVILLV 960
 DB 901 RLSEWIFRRVLYRPLYQIFGOIPLDEIDEARVNCSTHPLLEDSPSCSLYANMLVILLV 960

QY 961 TFLLVNTVLLNLLIAMFSYTFQVQGNADMFWKFORYNLIYVHERPALAPPFILLSHL 1020
 DB 961 TFLLVNTVLLNLLIAMFSYTFQVQGNADMFWKFORYNLIYVHERPALAPPFILLSHL 1020

QY 1021 SLTLRRVFKKEAEHKEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEH 1080
 DB 1021 SLTLRRVFKKEAEHKEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEH 1080

QY 1081 TAHRVDFIAKVLGGLREOEKRIKLESQINYSVLVSSVADVLAAQGGPRSSQHCGEQS 1140
 DB 1081 TAHRVDFIAKVLGGLREOEKRIKLESQINYSVLVSSVADVLAAQGGPRSSQHCGEQS 1140

QY 1141 LVAADHRGGLDGWEQPGAGQPPSDT 1165
 DB 1141 LVAADHRGGLDGWEQPGAGQPPSDT 1165

RESULT 2
 AAMS1708
 ID AAMS1708 standard; protein; 1165 AA.
 XX AAMS1708;
 AC AAMS1708;
 XX 16-JAN-2002 (first entry)
 DT Human TRP8.
 DE Mouse; human; TRP8; transient receptor potential channel;
 KW taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
 KW pharmaceutical.
 XX Homo sapiens.
 XX OS
 XX WO200179448-A2.
 XX 25-OCT-2001.
 XX 17-APR-2001; 2001WO-US012608.
 XX 17-APR-2000; 2000US-0197491P.
 XX 13-APR-2001; 2001US-00834792.
 XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX Margolske RF, Huang L, Rong M, Max M, Perez CA;
 XX MPI; 2002-017608/02.
 XX N-PSDB; AAI99708.
 XX A new transient receptor potential channel, designated TRP8, is expressed
 XX in taste receptor cells and associated with perception of bitter and
 XX sweet taste, and is useful to find new flavor enhancers.
 XX Claim 9; Fig 4; 55pp; English.
 XX The invention relates to a mouse and human transient receptor potential
 XX channel, TRP8, expressed in taste receptor cells and associated with the
 XX perception of bitter and sweet taste. Modulators of TRP8 are useful as
 XX flavour enhancers in foods, beverages and pharmaceuticals

SQ		Sequence 1165 AA;	
Query Match		100.0%; Score 6093; DB 5; Length 1165;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1165; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MQDVQPRGSGDADRELGHRGEVNPGGKRGKFRVPSGVAPSVLFDLLAEW	60
DB	1	MQDVQPRGSGDADRELGHRGEVNPGGKRGKFRVPSGVAPSVLFDLLAEW	60
QY	61	HLPAPLNVLVSGEOPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV	120
DB	61	HLPAPLNVLVSGEOPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV	120
QY	121	RHSLASTSTKRVVAVGMSALGRVLHRRILEBAQEDFPVHYPEDDGGSGPLCSLDSNL	180
DB	121	RHSLASTSTKRVVAVGMSALGRVLHRRILEBAQEDFPVHYPEDDGGSGPLCSLDSNL	180
QY	181	SHFILVEPPGKGDGLTELRLLEKHI SEORAGYGGTGSIEIPVLCILVNGDPNTLERI	240
DB	181	SHFILVEPPGKGDGLTELRLLEKHI SEORAGYGGTGSIEIPVLCILVNGDPNTLERI	240
QY	241	SRAVEQAAPWLLVVGSGGLADVLAALVNPHLLVPKVAEKQKPKSHFSEMEDIVRWT	300
DB	241	SRAVEQAAPWLLVVGSGGLADVLAALVNPHLLVPKVAEKQKPKSHFSEMEDIVRWT	300
QY	301	KLLQNTTSHQHLTVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDR	360
DB	301	KLLQNTTSHQHLTVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDR	360
QY	361	VDAKSEIFNGDVWKSCLDEEVMVDALVSNKPEFVRLFVNDGADVADFTLYGRLOELYR	420
DB	361	VDAKSEIFNGDVWKSCLDEEVMVDALVSNKPEFVRLFVNDGADVADFTLYGRLOELYR	420
QY	421	SVSRKSLLDLQKOEARELTLAGTQOAREPPAGPAFSLHVSRLVKDFLQDACHG	480
DB	421	SVSRKSLLDLQKOEARELTLAGTQOAREPPAGPAFSLHVSRLVKDFLQDACHG	480
QY	481	FYQDGRPGDRRAEKGFAKRPCTGOKMLLDLNKSENPRDLFLWVQLNRHEMATYFWAM	540
DB	481	FYQDGRPGDRRAEKGFAKRPCTGOKMLLDLNKSENPRDLFLWVQLNRHEMATYFWAM	540
QY	541	GOEGVAALAAACKILKEMSHLETEAPARATREAKYERLALDLFSECYSNSRPAFALV	600
DB	541	GOEGVAALAAACKILKEMSHLETEAPARATREAKYERLALDLFSECYSNSRPAFALV	600
QY	601	RNRNCWSKTTCLHLATEADAKFAHGDGVQAFILTRIMWGDMAAGTPIELLLGAFICPALV	660
DB	601	RNRNCWSKTTCLHLATEADAKFAHGDGVQAFILTRIMWGDMAAGTPIELLLGAFICPALV	660
QY	661	YTNLITFSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQGRGPRAVFL	720
DB	661	YTNLITFSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQGRGPRAVFL	720
QY	721	LTRWRKFGAPVTFLGNVVMYFAELFLTYVLLVDPRPPGSGPEVTLYFWVFTLV	780
DB	721	LTRWRKFGAPVTFLGNVVMYFAELFLTYVLLVDPRPPGSGPEVTLYFWVFTLV	780
QY	781	BEIROGFTFDETHLVKFTLVVGNWKNCDMVAIFLTVGVTCRMLPSAFAGRTVLAM	840
DB	781	BEIROGFTFDETHLVKFTLVVGNWKNCDMVAIFLTVGVTCRMLPSAFAGRTVLAM	840
QY	841	DMVFTLRLIHFALHKQLGPKIIVVERMKDVFVFFLFLSVMLVAYGVTTQALLHPHDG	900
DB	841	DMVFTLRLIHFALHKQLGPKIIVVERMKDVFVFFLFLSVMLVAYGVTTQALLHPHDG	900
QY	901	RLEWTFRRVLRYPIQIFQIPDEIDARVNCSTHPLLEDSPCPSLYANWLVILLV	960
DB	901	RLEWTFRRVLRYPIQIFQIPDEIDARVNCSTHPLLEDSPCPSLYANWLVILLV	960
QY	961	TFLLVTNVLNMLLTAMFSYTFQVQVGNADMFKQRYNLI VYHERPALAPFFILLSHL	1020
DB	961	TFLLVTNVLNMLLTAMFSYTFQVQVGNADMFKQRYNLI VYHERPALAPFFILLSHL	1020

1021 SLTLRRVFKAEHKKREHLERDLPLDOKVVTWETVQENFELSKMEKRDESEGEVLRK 1080

1021 SLTLRRVFKAEHKKREHLERDLPLDOKVVTWETVQENFELSKMEKRDESEGEVLRK 1080

1081 TAHRVDVFIKYLGLGLEQEKRIKLESQINYSVLVSSVADVLAAQGGGPRSSQHCGBGSQ 1140

1081 TAHRVDVFIKYLGLGLEQEKRIKLESQINYSVLVSSVADVLAAQGGGPRSSQHCGBGSQ 1140

1141 LVAADHRGGLDGWEOFGAGQPPSDT 1165

1141 LVAADHRGGLDGWEOFGAGQPPSDT 1165

RESULT 3

ABB83855

ID ABB83855 standard; protein; 1165 AA.

XX

AC ABB83855;

XX

DT 30-SEP-2002 (first entry)

XX

DE Human ltrpc6 SEQ ID NO 8.

XX

KW Human; ltrpc6; taste; cell signalling; TC-ICS; food; pharmaceutical;

XX

OS taste cell-specific ion channel subunit.

XX

PN Homo sapiens.

XX

WO200254069-A1.

XX

11-JUL-2002.

XX

26-DEC-2001; 2001WO-US049808.

XX

29-DEC-2000; 2000US-0259379P.

PR

21-DEC-2001; 2001US-00026188.

XX

(REGC) UNIV CALIFORNIA.

PA

Zuker CS, Zhang Y;

XX

WIPI; 2002-583632/62.

DR

N-PSDB; ABB85736.

XX

Identifying modulators of taste signaling in taste cells for use in food

PT

and pharmaceutical industries to customize and regulate taste, by

PT

determining effect of the compound on a taste cell-specific ion channel

PT

subunit.

XX

Claim 1; Page 305; 306pp; English.

PS

The invention relates to identifying (M1) a compound that modulates taste

CC

signalling in taste cells, by contacting the compound with a eukaryotic

CC

host cell or cell membrane which expresses a taste cell-specific ion

CC

channel subunit (TC-ICS), and determining a functional effect of the

CC

compound upon a transmembrane ion flux of a predetermined ion,

CC

identifying a compound that modulates taste signaling in taste cells.

CC

(M1) is useful for identifying a compound that modulates taste signalling

CC

in taste cells, for identifying a compound that binds to a taste cell

CC

specific ion channel subunit and for modulating taste signaling in taste

CC

cells of a mammal, in particular a human. Modulators identified by (M1)

CC

are used by the food and pharmaceutical industries to customize taste,

CC

e.g. as additives to food or medicine so that the food or medicine tastes

CC

different to the subject who ingests it. Bitter medicines can be made to

CC

taste less bitter and sweet substance can be enhanced. The modulators are

CC

useful for pharmacological and genetic modulation of taste signalling

CC

pathways. The taste modulators can be directly administered to mammalian

CC

subjects for modulation of taste in vivo. The present sequence is that of

CC

the predicted human ltrpc6 protein of the invention

XX

Sequence 1165 AA;

SQ

Query Match		100.0%; Score 6093; DB 5; Length 1165;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1165; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MDVQGPSPGDAEDRRLGLHRGVEVNGGSKKRGKFRVPSGVAPSVLPFLLLAEW	60
- Db	1	MDVQGPSPGDAEDRRLGLHRGVEVNGGSKKRGKFRVPSGVAPSVLPFLLLAEW	60
Qy	61	HLAPNLVSLVGEOPFAMKSWLRDLVLRKGLVKAOSTGAWILTSALRVLARHVGQAV	120
Db	61	HLAPNLVSLVGEOPFAMKSWLRDLVLRKGLVKAOSTGAWILTSALRVLARHVGQAV	120
Qy	121	RDHSLASTSTKRVVAVGMSLGRVLRHRRILEEAQEDFPVHYPEDDGGSQGLCSLDSNL	180
Db	121	RDHSLASTSTKRVVAVGMSLGRVLRHRRILEEAQEDFPVHYPEDDGGSQGLCSLDSNL	180
Qy	181	SHFILVSPGPKGGTGLTELRRLRLEKHSIORAGYGGTGSIEIPVLCILVNGDENTLERI	240
Db	181	SHFILVSPGPKGGTGLTELRRLRLEKHSIORAGYGGTGSIEIPVLCILVNGDENTLERI	240
Qy	241	SRVQQAAPMLILVSGGIADVLAAALVNPHLLVPKVAEKOFKEKFKSPKHSWEDIVRWT	300
Db	241	SRVQQAAPMLILVSGGIADVLAAALVNPHLLVPKVAEKOFKEKFKHSWEDIVRWT	300
Qy	301	KLLQNTSHQHLITVYDFEQSGSELDITVILKALVKACKSHSQBPQDYLDLKLAVADR	360
Db	301	KLLQNTSHQHLITVYDFEQSGSELDITVILKALVKACKSHSQBPQDYLDLKLAVADR	360
Qy	361	VDIAKSEIFNGDVWZKSCDLBEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELR	420
Db	361	VDIAKSEIFNGDVWZKSCDLBEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELR	420
Qy	421	SVSRSKSLFDLLQKQEBEARITLAGLGTQQAAREPPAGPPAPSLHEVSRVLKDFLQDAGR	480
Db	421	SVSRSKSLFDLLQKQEBEARITLAGLGTQQAAREPPAGPPAPSLHEVSRVLKDFLQDAGR	480
- Qy	481	FYQDGRGDRRAEKGPAKRTGQKWLDDLNKSENPRDRLFMAVLQNRHEMATYFWAM	540
Db	481	FYQDGRGDRRAEKGPAKRTGQKWLDDLNKSENPRDRLFMAVLQNRHEMATYFWAM	540
Qy	541	GOEGVAAALACKILKENSHELEAARAARATREAKYERLALDLFSECYNSSEARAFALLV	600
Db	541	GOEGVAAALACKILKENSHELEAARAARATREAKYERLALDLFSECYNSSEARAFALLV	600
Qy	601	RNRCSWKTCLHLATEADAKFAHGDVQAFPLTRIWMGDMAGTPILRLGAFICPALV	660
Db	601	RNRCSWKTCLHLATEADAKFAHGDVQAFPLTRIWMGDMAGTPILRLGAFICPALV	660
Qy	661	YTNLITPSEAPLRTGLDQLDLSLDTKSPLYGLQSRVRELVEAPRAQDGRGPRAVFL	720
Db	661	YTNLITPSEAPLRTGLDQLDLSLDTKSPLYGLQSRVRELVEAPRAQDGRGPRAVFL	720
Qy	721	LTRWRKFGAPVTYFLGNVVMYPAFLFTYVLLVDPRPPGPGSGPEVTLFYFWFTLVL	780
Db	721	LTRWRKFGAPVTYFLGNVVMYPAFLFTYVLLVDPRPPGPGSGPEVTLFYFWFTLVL	780
Qy	781	BEIROGFFDETHLVKFKFTLVGNWNKCDMVAIFLTVGVTCRMLPSAFAGRTVLAM	840
Db	781	BEIROGFFDETHLVKFKFTLVGNWNKCDMVAIFLTVGVTCRMLPSAFAGRTVLAM	840
Qy	841	DMVFTLRLIHTFAIKQLGPKIIIVVERMKDVFVFLPPLSVMLVAYGTTQALLPHDGH	900
Db	841	DMVFTLRLIHTFAIKQLGPKIIIVVERMKDVFVFLPPLSVMLVAYGTTQALLPHDGH	900
Qy	901	RLFWFRVLYPYLQIQOIPDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLIV	960
Db	901	RLFWFRVLYPYLQIQOIPDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLIV	960
Qy	961	TELLVTNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIYEHERPALAPFPILLSHL	1020
Db	961	TELLVTNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIYEHERPALAPFPILLSHL	1020
Qy	1021	SUTLRVFKKEAEHKEHLERDLDPDLDQKVVTWETVQKENFLSKMEKRERDSEGEVLRK	1080

Db	1021	SUTLRVFKKEAEHKEHLERDLDPDLDQKVVTWETVQKENFLSKMEKRERDSEGEVLRK	1080
Qy	1081	TAHRVDFIAKVLGGLREQEKRIKLESQINVCVLSVSVADVLAAQGGPRSSQHCGRGSQ	1140
Db	1081	TAHRVDFIAKVLGGLREQEKRIKLESQINVCVLSVSVADVLAAQGGPRSSQHCGRGSQ	1140
Qy	1141	LVAADHRGGLDGWEQPGAGQPPSDT	1165
Db	1141	LVAADHRGGLDGWEQPGAGQPPSDT	1165
RESULT 4			
ID	AAB86165	standard; protein; 1179 AA.	
XX	AAB86165;		
AC	AAB86165;		
XX	09-AUG-2001 (first entry)		
DT	09-AUG-2001 (first entry)		
XX	Human MTR1 protein.		
DE	Human MTR1 protein.		
XX	MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;		
KW	transient receptor potential family; BMS; Beckwith-Wiedemann syndrome;		
KW	lip15.5 abnormality; chromosome 11; anticancer; developmental activity;		
KW	intracellular calcium ion regulation; hormone; growth factor; apoptosis;		
KW	cell growth; cell death; cell differentiation; urogenital disease;		
KW	polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;		
KW	rhabdomyosarcoma.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO200132693-A2.		
PN	10-MAY-2001.		
XX	10-MAY-2001.		
PD	10-MAY-2001.		
XX	06-NOV-2000; 2000WO-DE003876.		
PF	06-NOV-2000; 2000WO-DE003876.		
XX	04-NOV-1999; 99DE-01053167.		
PR	04-NOV-1999; 99DE-01053167.		
XX	(UYGU-) UNIV GUTENBERG JOHANNES.		
PA	Prawitt D, Pelletier J, Zabel B;		
XX	WPI; 2001-316417/33.		
DR	DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann		
XX	syndrome and tumors, also related proteins and antibodies.		
PT	Disclosure; Fig 12; 46pp; German.		
XX	This invention describes a novel DNA sequence (I) encoding the MTR1		
CC	protein that: (i) has at least one biological activity of a TRP		
CC	(transient receptor potential) family protein; (ii) is connected with		
CC	etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected		
CC	with tumors involving lip15.5 abnormalities. The products of the		
CC	invention have anticancer and developmental activity. MTR1 is involved in		
CC	regulation of intracellular calcium ion levels, which are essential for		
CC	cellular responses to hormones and/or growth factors; also in apoptosis		
CC	and cell growth, death and differentiation, and in urogenital diseases,		
CC	including polycystic kidney disease. (I) and related ribozymes, antisense		
CC	RNA, proteins and antibodies (Ab) are used to treat or prevent diseases		
CC	associated with altered expression of the MTR1 gene or activity of its		
CC	protein, or with calcium influx into cells, e.g. BMS, Wilms tumor,		
CC	rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also		
CC	used for diagnosis of such diseases. (I) can also be used for recombinant		
CC	production of MTR1 proteins (II) (used for analysis, characterization and		
CC	therapy), as tissue or chromosomal markers, for identifying genetic		
CC	diseases and related sequences, as primers for genetic fingerprinting, as		
CC	source of oligonucleotides for biochips, and to raise anti-protein or		
CC	anti-DNA antibodies. (II) are used to raise Ab, as reagents in		
CC	competitive assays for (II), as tissue markers, for identifying		
CC	interacting proteins and in screening for (ant)agonists. This sequence		

CC represents a human MTR1 protein described in the method of the invention
 XX Query Match 99.0%; Score 6034; DB 4; Length 1179;
 SQ Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1162; Conservative 0; Mismatches 2; Indels 16; Gaps 3;

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QY 1 MQDVQGPSPGDAEDRRLGLHGEVNFVGGGKRGKFRVPSGVAPSVLPDLILAWE 60
DQ 1 MQDVQGPSPGDAEDRRLGLHGEVNFVGGGKRGKFRVPSGVAPSVLPDLILAWE 60
QY 61 HLPAPNLVSLVGEQPFAMKSHLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
DQ 61 HLPAPNLVSLVGEQPFAMKSHLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKRVAVAGMASLGRVLRHRRILEEAQEDFPVHYPPEDDGGSGPLCSLDSNL 180
DQ 121 RDHSLASTSTKRVAVAGMASLGRVLRHRRILEEAQEDFPVHYPPEDDGGSGPLCSLDSNL 180
QY 181 SHPILVEPPGPGDGLTELRLLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTLERI 240
DQ 181 SHPILVEPPGPGDGLTELRLLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTLERI 240
QY 241 SRAVEQAAPWLLVVGSGGIADVLAAALVNPQPHLLVPKVAEKQFKEKPPSKHFSWEDIVRWT 300
DQ 241 SRAVEQAAPWLLVVGSGGIADVLAAALVNPQPHLLVPKVAEKQFKEKPPSKHFSWEDIVRWT 300
QY 301 KLLQNTITSHQHLITVDVDFQEGSEELDTVLKALVKACKSHSOPDYLDLKLAVADR 360
DQ 301 KLLQNTITSHQHLITVDVDFQEGSEELDTVLKALVKACKSHSOPDYLDLKLAVADR 360
QY 361 VDIKSEIFNGDVWKSCLDEEVMDVLSNKPFFVRLFDVNGADVADFLTYGRQLQELVR 420
DQ 361 VDIKSEIFNGDVWKSCLDEEVMDVLSNKPFFVRLFDVNGADVADFLTYGRQLQELVR 420
QY 421 SVSRKSLFLDLQKQEEARLTLAGITQOAREPPAGPPAFSLHEVSRVLKDFLQACRG 480
DQ 421 SVSRKSLFLDLQKQEEARLTLAGITQOAREPPAGPPAFSLHEVSRVLKDFLQACRG 480
QY 481 FYQDGRPGDERRAEKGPAPKPTGQKWLDDLNKSENPRDLFLWAVLQNRHEMATYFWAM 540
DQ 481 FYQDGRPGDERRAEKGPAPKPTGQKWLDDLNKSENPRDLFLWAVLQNRHEMATYFWAM 540
QY 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERIAL-----DLFSECVSNSEARA 595
DQ 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERIAL-----DLFSECVSNSEARA 595
QY 596 FALLVRRNRCKWTKTCLHLATEADAKAFPAHDGVQAFILRIWGDMAAGTPIILRLGAPL 655
DQ 596 FALLVRRNRCKWTKTCLHLATEADAKAFPAHDGVQAFILRIWGDMAAGTPIILRLGAPL 655
QY 601 FALLVRRNRCKWTKTCLHLATEADAKAFPAHDGVQAFILRIWGDMAAGTPIILRLGAPL 659
DQ 601 FALLVRRNRCKWTKTCLHLATEADAKAFPAHDGVQAFILRIWGDMAAGTPIILRLGAPL 659
QY 656 CPALVYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRGP 715
DQ 656 CPALVYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRGP 715
QY 716 RAVFLTLTRKRWKFGAPVTVFLGNVVMYFAFLFTYVLIVDRPPPPQSGSEVTLTYFW 775
DQ 716 RAVFLTLTRKRWKFGAPVTVFLGNVVMYFAFLFTYVLIVDRPPPPQSGSEVTLTYFW 775
QY 776 FTLVLEETROGFTDETHLVKKFTLYVGDNNKCDMVAIFLPIVGVTCRMLPSFAEAGR 835
DQ 776 FTLVLEETROGFTDETHLVKKFTLYVGDNNKCDMVAIFLPIVGVTCRMLPSFAEAGR 835
QY 836 TVLAMDVWFTLRLTHIFAIHKQLGPKIIVVERMKDVFFFLFFLSVMLVAYGVTTQALL 895
DQ 836 TVLAMDVWFTLRLTHIFAIHKQLGPKIIVVERMKDVFFFLFFLSVMLVAYGVTTQALL 895
QY 896 HPDGRLEWIFRVLRYRPLVQIFQIPLDEIDAEARNVNSTHPLLEDGSPCSPLVYANVLV 955
DQ 896 HPDGRLEWIFRVLRYRPLVQIFQIPLDEIDAEARNVNSTHPLLEDGSPCSPLVYANVLV 955
QY 956 ILLLVTFLLVTVNLLMLLIAMFSYTFVQVQGNADMFWKFORNYLIVEYHERPALAPFFI 1015
  
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DQ 960 ILLLVTFLLVTVNLLMLLIAMFSYTFVQVQGNADMFWKFORNYLIVEYHERPALAPFFI 1019
QY 1016 LLSHLSLTLRRVPKKEA-----EHKREHLERDLDPDLQKVVTVETQKFNLSK 1065
DQ 1020 LLSHLSLTLRRVPKKEA-----EHKREHLERDLDPDLQKVVTVETQKFNLSK 1079
QY 1066 MEKRRDSEGEVLKTAHRVDFIAKVLGGREGEKRIKCLSEQINYSVLSSVADVLAQ 1125
DQ 1080 MEKRRDSEGEVLKTAHRVDFIAKVLGGREGEKRIKCLSEQINYSVLSSVADVLAQ 1139
QY 1126 GGGPRSSQHCQEGSQLVAADHRGGLDCWEQPGAGQPPSDT 1165
DQ 1140 GGGPRSSQHCQEGSQLVAADHRGGLDCWEQPGAGQPPSDT 1179

RESULT 5
AAB86164
ID AAB86164 standard; protein; 1158 AA.
XX
AC AAB86164;
XX
DT 09-AUG-2001 (first entry)
XX
DE Mouse MTR1 protein.
XX
KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW lip15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW cell growth; cell death; cell differentiation; urogenital disease;
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW rhabdomyosarcoma.
XX
OS Mus sp.
XX
PN WO200132693-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000MO-DE003876.
XX
PR 04-NOV-1999; 99DE-01053167.
XX
PA (UYGU-) UNIV GUTENBERG JOHANNES.
XX
PI Prawitt D, Pelletier J, Zabel B;
XX
DR WPI; 2001-316417/33.
XX
DR N-PSDB; AAH20623.
XX
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies.
XX
PS Disclosure; Fig 11; 46pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding the MTR1
CC protein that: (i) has at least one biological activity of a TRP
CC (transient receptor potential) family protein; (ii) is connected with
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving lip15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MTR1 is involved in
CC regulation of intracellular calcium ion levels, which are essential for
CC cellular responses to hormones and/or growth factors; also in apoptosis
CC and cell growth, death and differentiation, and in urogenital diseases,
CC including polycystic kidney disease. (I) and related ribozymes, antisense
CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
CC associated with altered expression of the MTR1 gene or activity of its
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC used for diagnosis of such diseases. (I) can also be used for recombinant
CC production of MTR1 proteins (II) (used for analysis, characterization and
CC therapy), as tissue or chromosomal markers, for identifying genetic
  
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CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (11) are used to raise Ab, as reagents in
 CC competitive assays for (11), as tissue markers; for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents the murine MTR1 gene described in the method of the invention
 . XX
 SQ Sequence 1158 AA;

Query Match 83.5%; Score 5088.5; DB 4; Length 1158;
 Best Local Similarity 84.1%; Pred. No. 0;
 Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MQDVQGRPGSGDAERELGLHGEVNFQSGKRGKRVFVSGVAPSVLFDLLAAEW 60
 Db 1 MQTTQSSCGPDPTEDEGWEPILCRGHINFGSGKRGKRVFVSGVAPSVLFDLLAAEW 60
 QY 61 HLPAPNLVSVLGEQPPAMKSWLRDLVRLKGLVKAAGSTGAWILTSALRVGLARHVGQAV 120
 Db 61 HLPAPNLVSVLGEERPLAMKSWLRDLVRLKGLVKAAGSTGAWILTSALRVGLARHVGQAV 120
 QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHYVEDDGGSGGPLCSLDS 178
 Db 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHYVEDDGGSGGPLCSLDS 180
 QY 179 NLSHFILVEPPGKGG--DGLTELRLRLKELHISEQAGYGGTGSIEIPVLCILVNGDPNTL 237
 Db 181 NLSHFILVESALGSGNDGLTELQSLSEKHLSQRTGYGGTSCIQIPVLCILVNGDPNTL 240
 QY 238 ERISRAVEQAAPWILVSGGDIADVLAAVNQPHLLVPKVAEKQKPEFSPKHSWEIV 297
 Db 241 ERISRAVEQAAPWILVSGGDIADVLAAVNQPHLLVPKVAEKQKPREFFPSECEFSWEIV 300
 QY 298 RWTLLQNTSHQHLITVYDFEORGSEELDTVILKALVKACKSHSQEPDQVLDLKLAVA 357
 Db 301 HWTLLQNTSHQHLITVYDFEORGSEELDTVILKALVKACKSHSQEPDQVLDLKLAVA 360
 QY 358 WDRVDIAKSEIFNGVDEWVKSCDLEBVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 417
 Db 361 WDRVDIAKSEIFNGVDEWVKSCDLEBVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 420
 QY 418 LVRSVRSKLLFDLLQKOEALRLTAGLGTQQAAREPPAGPPAFSLHEVSRVLDKFLQDA 477
 Db 421 LVHSVSPKSLPELLQKHEEGLTLAGLGAQAARELPGLPAFSLHEVSRVLDKFLQDA 480
 QY 478 CRGFYQDGG----RRMEERGPVKRPAQKWLPLSRKSEDPWDLFLWVQLNHEWATVF 537
 Db 481 CRGFYQDGG----RRMEERGPVKRPAQKWLPLSRKSEDPWDLFLWVQLNHEWATVF 536
 QY 538 WAMQGVGAALAAACKILKEMSHLETEAFAARATREAKYERIALDLFSECYSNSBARAPA 597
 Db 537 WAMQGVGAALAAACKILKEMSHLETEAFAARATREAKYERIALDLFSECYSNSBARAPA 596
 QY 598 LLVRRNRCKWTKTCLHATEADAKFAHGDGVAQFLTRVWGDMAAGTPIELLLGAFCLCP 657
 Db 597 LLVRRNRCKWTKTCLHATEADAKFAHGDGVAQFLTRVWGDMAAGTPIELLLGAFCLCP 656
 QY 658 ALVYTNLITFSEAPLRTGLELDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQGRGPRA 717
 Db 657 ALVYTNLITFSEAPLRTGLELDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQGRGPRA 716
 QY 718 VFLLTRWRKFWGAPVTVFVGNVVMYFAFLFTYVLLVDVFRPPPPQSPGPEVTLFYWVFT 777
 Db 717 VFLLTRWRKFWGAPVTVFVGNVVMYFAFLFTYVLLVDVFRPPPPQSPGPEVTLFYWVFT 776
 QY 778 LVLEETRQGFTEDETHLVKKTLYVGNWKNCDMVAIFLFTVGTVTCMLPSAFAEAGRTV 837
 Db 777 LVLEETRQGFTEDETHLVKKTLYVGNWKNCDMVAIFLFTVGTVTCMLPSAFAEAGRTV 836
 QY 838 LAMDEWVFTLRLHIFAIHKQGPXKIIIVVERWMDVFFFLFLLSVMLVAYGVTQTALLHP 897
 Db 837 LAMDEWVFTLRLHIFAIHKQGPXKIIIVVERWMDVFFFLFLLSVMLVAYGVTQTALLHP 896

QY 898 HDGRLEWIFRRVLYRPLVLIQIFGOIPLEIDIEARVNCSTHPILEDSPSCPSLVANLVIL 957
 Db 897 HDGRLEWIFRRVLYRPLVLIQIFGOIPLEIDIEARVNCSTHPILEDSPSCPSLVANLVIL 956
 QY 958 LLVTELLVTVLMLNLLIAMFSYTFVQVQGNADMFQKFORNYLIVEYHERPALAPFPILL 1017
 Db 957 LLVTELLVTVLMLNLLIAMFSYTFVQVQGNADMFQKFORNYLIVEYHERPALAPFPILL 1016
 QY 1018 SHLSLTLRRVFKKEAEHREHLERDLPDLDQKQVVTWETVQKENFLSKMKRRRDSGEV 1077
 Db 1017 SHLSLVLKQVFRKEAQHQRHLERDLPDLDQKQVVTWETVQKENFLSKMKRRRDSGEV 1076
 QY 1078 LRKTAHRVDIAKYLGLRQEKRIKLESQINQSVLGSVADVLQAGGSPRSSQHCGE 1137
 Db 1077 LRKTAHRVDIAKYLGLRQEKRIKLESQINQSVLGSVADVLQAGGSPRSSQHCGE 1136
 QY 1138 GSQVLAADHRGGLDGEQPGAGQPPSDT 1165
 Db 1137 RSQPASARDREYLE-----SGLFPST 1158

RESULT 6
 ABB83854
 ID ABB83854 standard; protein; 1158 AA.
 AC ABB83854;
 DT 30-SEP-2002 (first entry)
 DE Mouse ltrpc5 SEQ ID NO 5.
 KW Mouse; ltrpc5; taste; cell signalling; TC-ICS; food; pharmaceutical;
 taste cell-specific ion channel subunit.
 OS Mus sp.
 PN WO200254069-A1.
 PD 11-JUL-2002.
 PF 26-DEC-2001; 2001WO-US049808.
 PR 29-DEC-2000; 2000US-0259379P.
 PR 21-DEC-2001; 2001US-00026188.
 XX (REGC) UNIV CALIFORNIA.
 PA Zuker CS, Zhang Y;
 PI
 XX WPI; 2002-583632/62.
 DR N-PSDB; ABB85734.
 XX
 PT Identifying modulators of taste signaling in taste cells for use in food
 PT and pharmaceutical industries to customize and regulate taste, by
 PT determining effect of the compound on a taste cell-specific ion channel
 PT subunit.
 PS Claim 1; Page 211; 306pp; English.
 CC The invention relates to identifying (M1) a compound that modulates taste
 CC signalling in taste cells, by contacting the compound with a eukaryotic
 CC host cell or cell membrane which expresses a taste cell-specific ion
 CC channel subunit (TC-ICS), and determining a functional effect of the
 CC compound upon a transmembrane ion flux of a predetermined ion.
 CC Identifying a compound that modulates taste signalling in taste cells.
 CC (M1) is useful for identifying a compound that binds to a taste cell
 CC in taste cells, for identifying a compound that modulates taste signalling
 CC specific ion channel subunit and for modulating taste signalling in taste
 CC cells of a mammal, in particular a human. Modulators identified by (M1)
 CC are used by the food and pharmaceutical industries to customize taste,
 CC e.g. as additives to food or medicine so that the food or medicine tastes
 CC different to the subject who ingests it. Bitter medicines can be made to
 CC taste less bitter and sweet substance can be enhanced. The modulators are

CC useful for pharmacological and genetic modulation of taste signalling
CC pathways. The taste modulators can be directly administered to mammalian
CC subjects for modulation of taste in vivo. The present sequence is that of
CC the predicted mouse *ltrpc5* protein of the invention
XX
SQ Sequence 1158 AA;

Query Match 83.5%; Score 5088.5; DB 5; Length 1159;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY	1	MDVQGGPRPGDABDRRELGLHRGEVNFSGSGKKRGKRVFVPSGVAPSVLFDLLLAEW	60
Db	1	MQTTQSSCPGSPDPDTEGWEPILCRGEINFCGSGKKRGKRVKVPSSVAPSVLFEILLTEW	60
QY	61	HLPAPNLVSLVGEQPFAMKSWLVDVLKGLVKAAQSTGAWIITSAUVGLARHVGOAV	120
Db	61	HLPAPNLVSLVGBERPLAMKSWLVDVLKGLVKAAQSTGAWIITSAUVGLARHVGOAV	120
QY	121	RDHSLASTSTKRVVAVGMASLGRVLHRRILE--EAQEDFPHVYBEDDGGSGPCLSLDS	178
Db	121	RDHSLASTSTKRVVAVGMASLGRVLHRRILE--EAQEDFPHVYBEDDGGSGPCLSLDS	180
QY	179	NLSHFILVEPPGKG-DGLTEFLRLKXHSIQORAGYGGTGSTYEIPVLCILVNGDPNTL	237
Db	181	NLSHFILVESGALGSGNDGLTELQSLSEKHSIQORTGYGGTSCIOIPVLCILVNGDPNTL	240
QY	238	ERISRAVEQAAPMLILVSGGGIADVLAAVNQPHLLVPKVAEKFKFKFSKHFWSWDIV	297
Db	241	ERISRAVEQAAPMLILAGSGGIADVLAAVSPQPHLLVPQVAEKFKFKFSECFSEWAIV	300
QY	298	RWTKLLQNISSHOLLTVYDPEOBGSEBELDTVILKALVKACKSHSQBPQDYLDLKLAVA	357
Db	301	HWTELLONIAAHPHLLTVYDPEOBGSEBELDTVILKALVKACKSHSQBPQDYLDLKLAVA	360
QY	358	WDRVDIAKSIIFNGDVEWKSCDLEEVNMVDALVSNKPEFVRLFVDNGADVADFITYGRLQE	417
Db	361	WDRVDIAKSIIFNGDVEWKSCDLEEVNMTDALVSNKPDFVRLFVDSGADMAEFLLTYGRLQQ	420
QY	418	LYRSVSRKSLFLDLLQKQBEARITLAGLGTQQAAREPPAGPPAPFSLHEVSRLVKDFLQDA	477
Db	421	LYHSVSPKSLFLFELLQKHEEGRITLAGLGAQQAARELPGLGPAFSLHEVSRLVKDFLHDA	480
QY	478	CRGFYQDGRPGDRRAEKGPAKPTQKQWLDDLNQKSENPRWDLFLMAVILQNRHEMATYF	537
Db	481	CRGFYQDG----RMEERGGPKRPAQKQWLPDLRSKSDPWRDLFLMAVILQNRHEMATYF	536
QY	538	WAMQOEGVAAALAAKILKMSHLETAEBARATREAKYERLALDLPSECYSNSSEARAF	597
Db	537	WAMRGVAAALAAKILKMSHLEKEAEVARTWREAKYEQALDLPSECYGNSSEARAF	596
QY	598	LLVRRNRCWSKITCLHLATEADAKAFHHDGVOAFLTRIWWGDMAAGTPIRLLLGAFLCP	657
Db	597	LLVRRNHSRITCLHLATEADAKAFHHDGVOAFLTKIWWGDMAAGTPIRLLLGAFTCP	656
QY	658	ALVYTNLIITSEBAPRTGLIEDLQDLDEKSPYGLQSRVEELVEAPRAQDGRGPA	717
Db	657	ALVYTNLIISFSEDAPQRMDELDLQEPDSDLMEXSFLCSRGQGLKLETEAPRAPDGLGPA	716
QY	718	VFLLTWRKFWGAPVTELGNNVYMAFLFLFTYVILLVDRPPPPQSGSGEVTLYFWVFT	777
Db	717	AFLLTWRKFWGAPVTELGNNVYMAFLFLFTYVILLVDRPPPPQSGSGEVTLYFWVFT	776
QY	778	LVLEEIIRQGFDTEDHLVKKFTLYVGDNNWNCMDVAIFLFIYGVTCRMLPSAFEAGRTV	837
Db	777	LVLEEIIRQGFDTEDHLVKKFTLYVEDNWNKCMDVAIFLFIYGVTCRWWPVSFEAGRTV	836
QY	838	LAMDWMVFTLRLLHIFAIHKQLGPKIIVVERMMKQDVFFFLFSLVMLVAYGVTTQALLHP	897
Db	837	LAIDWMVFTLRLLHIFAIHKQLGPKIIVVERMMKQDVFFFLFSLVMLVAYGVTTQALLHP	896
QY	898	HQGRLEWIFRRVLRYRPLQIFQOIPLDIDEARVNCSTHPLLDEDSFCSPLYANLWVIL	957

RESULT 7

AA86166	
ID	AA86166 standard; protein; 1158 AA.
XX	
AC	AA86166;
XX	
DT	09-AUG-2001 (first entry)
XX	
DE	Mouse MTR1 protein #2.
XX	
KW	MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW	transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW	11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW	intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW	cell growth; cell death; cell differentiation; urogenital disease;
KW	polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW	rhabdomyosarcoma.
XX	
OS	Mus sp.
XX	
WO	2001032693-A2.
PN	
XX	
PD	10-MAY-2001.
XX	
PF	06-NOV-2000; 2000WO-DE003875.
XX	
PR	04-NOV-1999; 99DE-01053167.
XX	
PA	(UYGU-) UNIV GUTENBERG JOHANNES.
XX	
PI	Prawitt D, Pelletier J, Zabel B;
XX	
DR	WPI; 2001-316417/33.
XX	
DT	DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
PT	syndrome and tumors, also related proteins and antibodies.
XX	
PS	Disclosure; Fig 12; 46pp; German.
XX	
CC	This invention describes a novel DNA sequence (I) encoding the MTR1
CC	protein that: (i) has at least one biological activity of a TRP
CC	(transient receptor potential) family protein; (ii) is connected with
CC	etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC	with tumors involving 11p15.5 abnormalities. The products of the
CC	invention have anticancer and developmental activity. MTR1 is involved in
CC	regulation of intracellular calcium ion levels, which are essential for
CC	cellular responses to hormones and/or growth factors; also in apoptosis
CC	and cell growth, death and differentiation, and in urogenital diseases,
CC	including polycystic kidney disease. (I) and related ribozymes, antisense
CC	RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
CC	associated with altered expression of the MTR1 gene or activity of its
CC	protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC	rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC	used for diagnosis of such diseases. (I) can also be used for recombinant

CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers; for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents the murine MTR1 gene described in the method of the invention
 XX
 XX

Sequence 1158 AA;

Query Match 83.4%; Score 5080.5; DB 4; Length 1158;
 Best Local Similarity 84.0%; Pred. No. 0;
 Matches 981; Conservative 67; Mismatches 107; Indels 13; Gaps 4;

QY 1 MDVQGPFGDAEDRRLGLHGEVNFSGSKKGFVRVPSGVAPSVLFOLLAEW 60
 DB 1 MDTQSSCGFPPDTEGWEPILCRGEINFGSGKGRKFKVFPSSVAPSVLFELLTEW 60
 QY 61 HLPAPNLVSVLGEOPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVGLARHVQAV 120
 DB 61 HLPAPNLVSVLGEOPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVGLARHVQAV 120
 QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--BAQEDFPVHPEDDGGSGQPLCSLDS 178
 DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--BAQEDFPVHPEDDGGSGQPLCSLDS 178
 QY 179 NLSHFILVEPPGKG-DGLTELRRLRLEKHISEQAGYGGTGSIEIPVLCILVNGDPNTL 237
 DB 181 NLSHFILVESGALSGNDGLTELQSLSEKHISQRTGYGGTSCIPIVLCILVNGDPNTL 240
 QY 238 ERISRAVQAPWLLTVGSGGIADVLAALVNOPHLLVPKVAEKQFKFPSPKHSFWEIV 297
 DB 241 ERISRAVQAPWLLTVGSGGIADVLAALVNOPHLLVPKVAEKQFKFPSPKHSFWEIV 297
 QY 298 RWTCLQNTSHQHLTYVDFEQESBELDTVILKALVKACKSHSQEPDYLDLKLAVA 357
 DB 301 HWTCLQNTSHQHLTYVDFEQESBELDTVILKALVKACKSHSQEPDYLDLKLAVA 360
 QY 358 WDRVDIAKSEIFNGDVEWKSCLDEVMVDALVSNKPEFVRLPVDNGADVADFLTVGRLOE 417
 DB 361 WDRVDIAKSEIFNGDVEWKSCLDEVMVDALVSNKPEFVRLPVDNGADVADFLTVGRLOE 420
 QY 418 LYRSVRSKSLPDLILQKQBEARLTLAGTQOAREPPAGPPAFSLHEVSRVLKDFLODA 477
 DB 421 LYHSVSPKSLPDLILQKQBEARLTLAGTQOAREPPAGPPAFSLHEVSRVLKDFLODA 480
 QY 478 CRGFYQDGRPDRRAEAKGPAKPTGQKWLIDNOKSENPDRLFLMAVLQNHMATYF 537
 DB 481 CRGFYQDGRPDRRAEAKGPAKPTGQKWLIDNOKSENPDRLFLMAVLQNHMATYF 536
 QY 538 WAMQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAPA 597
 DB 537 WAMQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAPA 596
 QY 598 LLVRRNRCKWTKTCLHLATEADAKFAFFHDGVQAFILRIWGDMAAGTPIRLLLGAFLCP 657
 DB 597 LLVRRNRCKWTKTCLHLATEADAKFAFFHDGVQAFILRIWGDMAAGTPIRLLLGAFLCP 656
 QY 658 ALVYTNLTIFSEAPRTGLDLDLSDTEKSPYGLQSRVEELVEAPRAGRCPPA 717
 DB 657 ALVYTNLTIFSEAPRTGLDLDLSDTEKSPYGLQSRVEELVEAPRAGRCPPA 716
 QY 718 VFLLTWRKFWGAPVTVLGNVMVFAFLFTYLLVDFRPPPGSPGPEVTLVFWVFT 777
 DB 717 AFLLTWRKFWGAPVTVLGNVMVFAFLFTYLLVDFRPPPGSPGPEVTLVFWVFT 776
 QY 778 LVLEIRIQGFPTDTHLVKKTFLYVGDNNKCDMVAIFLIVGVTCRMLPSAFAGRTV 837
 DB 777 LVLEIRIQGFPTDTHLVKKTFLYVGDNNKCDMVAIFLIVGVTCRMLPSAFAGRTV 836
 QY 838 LAMDEWVFTLRLLIHI FAHKQLGPKLIIVVERMMKDVFFFLFSLVWLVAVGTTQALLHP 897

DB 837 LAIDEMVFTLRLLIHI FAHKQLGPKLIIVVERMMKDVFFFLFSLVWLVAVGTTQALLHP 896
 QY 898 HDGRLEWIFRRVLYRYPYLIQIFGQIPLEIDEARVNCSTHPLLEDSPSCPSLYANWLVL 957
 DB 897 HDGRLEWIFRRVLYRYPYLIQIFGQIPLEIDEARVNCSTHPLLEDSPSCPSLYANWLVL 956
 QY 958 LLVTFLLVTVNLLNLLIAMFSYTFQVVOGNADMFVFORNLIVEHSPALAPPFILL 1017
 DB 957 LLVTFLLVTVNLLNLLIAMFSYTFQVVOGNADMFVFORNLIVEHSPALAPPFILL 1016
 QY 1018 SHLSLTLRRVPKKEAHRHLERLDPDLDDKVVVTWETVOKENFLGKMKRRRDSGEV 1077
 DB 1017 SHLSLTLRRVPKKEAHRHLERLDPDLDDKVVVTWETVOKENFLGKMKRRRDSGEV 1076
 QY 1078 LRKTAHRVDFIAKYLGLRQEKIKCLESQINYSVSVADVLAQGGGPRSSQHCGE 1137
 DB 1077 LRKTAHRVDFIAKYLGLRQEKIKCLESQINYSVSVADVLAQGGGPRSSQHCGE 1136
 QY 1138 GSQVLVADHRGGLDGWEPQAGQPPSDT 1165
 DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 8
 AAM51707
 ID AAM51707 standard; protein; 1157 AA.
 XX
 AC AAM51707;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Mouse TRP8.
 KW Mouse; human; TRP8; transient receptor potential channel;
 KW taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
 KW pharmaceutical.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 467
 FT /note= "Encoded by CACGAG"
 XX
 PN WO200179448-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US012608.
 PR 17-APR-2000; 2000US-0197491P.
 PR 13-APR-2001; 2001US-00834792.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Margolskee RF, Huang L, Rong M, Max M, Perez CA;
 XX
 PI WPI; 2002-017608/02.
 DR N-PSDB; AAI99707.
 DR
 XX
 PT A new transient receptor potential channel, designated TRP8, is expressed
 PT in taste receptor cells and associated with perception of bitter and
 PT sweet taste, and is useful to find new flavor enhancers.
 XX
 PS Claim 8; Fig 2; 55pp; English.
 XX
 CC The invention relates to a mouse and human transient receptor potential
 CC channel, TRP8, expressed in taste receptor cells and associated with the
 CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
 CC flavour enhancers in foods, beverages and pharmaceuticals
 XX
 SQ Sequence 1157 AA;

Query Match

83.3%; Score 5073; DB 5; Length 1157;

Best Local Similarity 84.0%; Pred. No. 0;
Matches 981; Conservative 67; Mismatches 106; Indels 14; Gaps 5;

QY 1 MQVQGRPGSPGDAERRELGLHGRVNFVGGSKGKFKVRVPSGVAPSVLPDLILAEW 60
DB 1 MQTQSCPCSPPTDEGWBPILCRGHNFGGSKGKFKVFPSSVAPSVLPFELLTEW 60
QY 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRGLARHVGOAV 120
DB 61 HLPAPNLVSLVGERPLANKSWLRDLVRKGLVKAAQSTGAWILTSALHVLARHVGOAV 120
QY 121 RDHSLASTSKVRVWAGMASLGRVLRHRRILE--EAQEDFPVHYDPDDGGSGQPLCLSDS 178
DB 121 RDHSLASTSKIRVVAIGMASLGRILRQLLDGWHQKEDTPIHYPADEGNIQGPLCLDLS 180
QY 179 NLGSHFVLVEPGPGKG-DGLTELRLRLKHI SEORAGYGGTGTIEIVLCLLVNGDNTL 237
DB 181 NLGSHFVLVESALGSGNDGTELGSLKHI SQRTGYGGTGTCTQIPVLCVVNGDNTL 240
QY 238 ERISRAVEQAAPMLILVGGGIAADVLAALVNPQHLVPKVAEQKFKFSPKHSFWSWDIV 297
DB 241 ERISRAVEQAAPMLILAGSGGIAADVLAALVNPQHLVPKVAEQKFKFSECFSEWAI 300
QY 298 RWTLLQNTLSHOLLTVYDFEGBGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVA 357
DB 301 HWTLLQNTAAHPHLLTVYDFEGBGSEELDTVILKALVKACKSHSQEAQDYLDLKLAVA 360
QY 358 WDRVDIAKSEIFNGDVEWKSCLDEEVMDALVNKPEFVRLFVDNGADVADFTLYGRLOE 417
DB 361 WDRVDIAKSEIFNGDVEWKSCLDEEVMDALVNKPEFVRLFVDNGADMAEFYTYGRLOQ 420
QY 418 LVRSVRSKSLLLFOLLQKOEALRTLAGLTQOAREPPAGPPAFSLHEVSRVLKDFLQDA 477
DB 421 LVHSVSPKSLFELLQKHEBGLTLAGLGAQARELPGLPAFSLH-VSRVLKDFLHDA 479
QY 478 CRGYODGRPGDERRAEKPAKPTQKWLLDLNQKSENPWRDLFWAVLQNRHEMATYF 537
DB 480 CRGYODG---RRMEERPGPKPAGQKWLPLDSRKSDEPWRDLFWAVLQNRHEMATYF 535
QY 538 WAMQGVGAALAAACKILKEMSHLETEAARAATREAKYERLALDLSFECYSSEARAFA 597
DB 536 WAMGREGVAAALAAACKIIEKMSHLEKEAEVARTMREAKYEQALDLDLSFECYGNSEDRARA 595
QY 598 LLVRRNRCKSTCLHLATEADAKAFHAGDVGQAFTRIWWGDMAGTPTILRLGAFLOCP 657
DB 596 LLVRRNHSRTTCLHLATEADAKAFHAGDVGQAFTRIWWGDMAGTPTILRLGAFLOCP 655
QY 658 ALVYTNLTFSSEAPLRTGLELDLSDLTDEKSPLYGLQSRVEELVEAPRAGQGRGPA 717
DB 656 ALIYTNLTFSSEAPLRTGLELDLSDLTDEKSPLYGLQSRVEELVEAPRAGQGRGPA 715
QY 718 VFLLTRWRKFWGAPVTVFLGNVVMVPAFLFTYVLLVDFRPPPGSPGPEVTLVFWVFT 777
DB 716 AFLTRWRKFWGAPVTVFLGNVVMVPAFLFTYVLLVDFRPPPGSPGSEVTLVFWVFT 775
QY 778 LVLEIRQGFDETHLVKFTLYVGDNNKCDMVAIFLFTVGVTCRMLPSAFAGRTV 837
DB 776 LVLEIRQGFDETHLVKFTLYVEDNNKCDMVAIFLFTVGVTCRMLPSAFAGRTV 835
QY 838 LAMDFWVFTLRILHIFATHKQIGPKIIVVERMKDVFFLPFLSVLWVAYGVTTOALLHP 897
DB 836 LAIDFWVFTLRILHIFATHKQIGPKIIVVERMKDVFFLPFLSVLWVAYGVTTOALLHP 895
QY 898 HDGRLEWIFRRVLYRPIYQIFQIPLDEIDEARVNCSTHPLLEDPSCPSIYANWLVIL 957
DB 896 HDGRLEWIFRRVLYRPIYQIFQIPLDEIDEARVNCSTHPLLEDPSCPSIYANWLVIL 955
QY 958 LLVTELLVTNLLMNLIAFSTYQVQGNADMEFWKFORNYLIVEYHERPALAPFFILL 1017
DB 956 LLVTELLVTNLLMNLIAFSTYQVQGNADMEFWKFORNYLIVEYHERPALAPFFILL 1015
QY 1018 SHLSLTLRVRFKAEHREHLERDLPDLQKVTVTWQENFLSKVMEKRRDSEGEV 1077
DB 1018 SHLSLTLRVRFKAEHREHLERDLPDLQKVTVTWQENFLSKVMEKRRDSEGEV 1077

Db 1016 SHLSVLVKQVFRKBAHQHRLERDLPDLQKIIITWQENFLSKVMEKRRDSEGEV 1075
QY 1078 LRKTAHRVDIAKYLGLRQEKRIKLESQINVCVSVLVSVADVLAQGGGFRSSQHGE 1137
DB 1076 LRKTAHRVDIAKYLGLRQEKRIKLESQINVCVSVLVSVADVLAQGGGFRSSQHGE 1135
QY 1138 GSQLVAAADHRGGDLGWEPGCGAGOPPSPDT 1165
DB 1136 RSQFASAREYLE-----SGLPPSDT 1157

RESULT 9
ABB83853
ID ABB83853 standard; protein; 1164 AA.
XX ABB83853;
AC ABB83853;
XX 30-SEP-2002 (first entry)
XX Rat L-TRP SEQ ID NO 2.
DE Rat; L-TRP; taste; cell signalling; TC-ICS; food; pharmaceutical;
KW taste cell-specific ion channel subunit.
XX Rattus sp.
XX WO200254069-A1.
XX 11-JUL-2002.
XX 26-DEC-2001; 2001WO-US049808.
XX 29-DEC-2000; 2000US-0259379P.
XX 21-DEC-2001; 2001US-00026188.
XX (REGC) UNIV CALIFORNIA.
XX Zuker CS, Zhang Y;
XX WPI; 2002-583632/62.
XX N-PSDB; ABB85732.
XX Identifying modulators of taste signaling in taste cells for use in food
PT and pharmaceutical industries to customize and regulate taste, by
PT determining effect of the compound on a taste cell-specific ion channel
PT subunit.
XX Claim 1; Page 63; 306pp; English.
XX The invention relates to identifying (M1) a compound that modulates taste
CC signalling in taste cells, by contacting the compound with a eukaryotic
CC host cell or cell membrane which expresses a taste cell-specific ion
CC channel subunit (TC-ICS), and determining a functional effect of the
CC compound upon a transmembrane ion flux of a predetermined ion,
CC identifying a compound that modulates taste signaling in taste cells.
CC (M1) is useful for identifying a compound that modulates taste signalling
CC in taste cells, for identifying a compound that binds to a taste cell
CC specific ion channel subunit and for modulating taste signaling in taste
CC cells of a mammal, in particular a human. Modulators identified by (M1)
CC are used by the food and pharmaceutical industries to customize taste
CC e.g. as additives to food or medicine so that the food or medicine tastes
CC different to the subject who ingests it. Bitter medicines can be made to
CC taste less bitter and sweet substance can be enhanced. The modulators are
CC useful for pharmacological and genetic modulation of taste signalling
CC pathways. The taste modulators can be directly administered to mammalian
CC subjects for modulation of taste in vivo. The present sequence is that of
CC the rat L-TRP protein of the invention
XX Sequence 1164 AA;
SQ

Query Match 82.2%; Score 5008.5; DB 5; Length 1164;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 965; Conservative 77; Mismatches 113; Indels 11; Gaps 3;

QY 1 MQDVQPRPGSGDAEDRRRLGLHGEVNFVGGSKKRGKVRVPVSGVAPSVLPDLILAEW 60
Db 9 MPMAQSSCPGSPPTDGTGWEVFLCVGEVNFVGGSKKRGKVRVPVSGVAPSVLPDLILAETW 68
QY 61 HLPAPNLVSVLGEQPFAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
Db 69 HLPAPNLVSVLGEERLFAKMSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGOAV 128
QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRLLEAEQEDPVHYPEDDGSQCPGLCSLDSNL 180
* Db 129 RDHSLASTSTKRVVAVGMSLGRVLRHRLLEAEQEDPVHYPEDDGSQCPGLCSLDSNL 188
QY 181 SHFTLVEPGPKGK-DGTELRRLKLEKHSORAGYGGTGIETIIPVCLLVNGDPNTLER 239
Db 189 SHFTLVEPGTUGSGNDGLAEQLSLEKHSORAGYGGTGIETIIPVCLLVNGDPNTLER 248
QY 240 ISRAVEQAAPMLILVGGGIAADVLAAALVNPQHLVPAKVAEKQFKEKFPSEKHSFMSDEIVRW 299
Db 249 MSRAVEQAAPMLILVGGGIAADVLAAALVNPQHLVPAKVAEKQFKEKFPSEKHSFMSDEIVRW 308
QY 300 TKLQNTTSHOHLITVDFEGSGEELDTVILKALVKAACKSHSQBPQDYLDELKLA VAWD 359
Db 309 TELQNTIAHPHLLITVDFEGSGEELDTVILKALVKAACKSHSQBPQDYLDELKLA VAWD 368
QY 360 RVDIAKSIIFNGDVEWKCDEEVMVDALVSNKPEFVRLFVNDGADVADFLTIGRLOELY 419
Db 369 RVDIAKSIIFNGDVEWKCDEEVMVDALVSNKPEFVRLFVNDGADVADFLTIGRLOELY 428
QY 420 RSVRSKSLFLLQKQBEARLTLAGLTQQAAREPPAGPAPFSLHEVSRVLKDFLODACR 479
Db 429 HVSVPKSLFELLERKEEGRLLTAGLGAQQTAKLPAFVGLPAFSLHEVSRVLKDFLODACR 488
QY 480 GYQDGRGDRRAEKGAKPTGOKWLLDNLKSENKPRDLFTWAVLQNRHEMATYFWA 539
Db 489 GYQDGRGDRRAEKGAKPTGOKWLLDNLKSENKPRDLFTWAVLQNRHEMATYFWA 544
QY 540 MGOEGVAALAAACKILKEMSHLETAEAARAYREAKYERLALDLFSECVSNSEARAFALL 599
Db 545 MREGVAALAAACKILKEMSHLETAEAARAYREAKYERLALDLFSECVSNSEARAFALL 604
QY 600 VRNRCSKTTCLHLATEADAKAFPAHGVQAFPLTRIMWGMMAAGTPILRLGAFCLPAL 659
Db 605 VRNRCSKTTCLHLATEADAKAFPAHGVQAFPLTRIMWGMMAAGTPILRLGAFCLPAL 664
QY 660 VTNLITSEAPLATGLEDLQDLSLDEKSPLYGLQSRVLEAPRAQDGRPAFV 719
Db 665 IYTNLITSEAPLATGLEDLQDLSLDEKSPLYGLQSRVLEAPRAQDGRPAFV 724
QY 720 LLTRWRKFGAPVTFLGNVVMYFAPFLFTYVLLVDFRPPQPGSGPEVTLYFWVFTLV 779
Db 725 LLTRWRKFGAPVTFLGNVVMYFAPFLFTYVLLVDFRPPQPGSGPEVTLYFWVFTLV 784
QY 780 LBEIRQGPFTDTHLVKFKFTLYVGNWKNKCDMVAIFLIVGVTCEMLPSAFAEAGTVLA 839
Db 785 LBEIRQGPFTDTHLVKFKFTLYVGNWKNKCDMVAIFLIVGVTCEMLPSAFAEAGTVLA 844
QY 840 MDPMVFTLRIHFAHKLQGPKIIVVERMKDVRPFLEFLSVLWVAYGVTTQALLPHD 899
Db 845 IDPMVFTLRIHFAHKLQGPKIIVVERMKDVRPFLEFLSVLWVAYGVTTQALLPHD 904
QY 900 GRLEWIFRVLRYPLQIFQIQLDDEIDARVNCSTHPLLEDSPSCPSLYANWLVILL 959
Db 905 GRLEWIFRVLRYPLQIFQIQLDDEIDARVNCSTHPLLEDSPSCPSLYANWLVILL 964
QY 960 VTFLLVNTVLLMILLIAMSYFQVQGNADMFQKQRYNLIVYHERPALAPPFTLLSH 1019
Db 965 VTFLLVNTVLLMILLIAMSYFQVQGNADMFQKQRYNLIVYHERPALAPPFTLLSH 1024
QY 1020 LSLTLARVFKAEHKEHRLERDLPDQKQVVTWETVQENKFLSKMKRRRSEGEVLR 1079
Db 1025 LSLTLARVFKAEHKEHRLERDLPDQKQVVTWETVQENKFLSKMKRRRSEGEVLR 1084

QY 1080 KTAHRVDIAKYLGGLREQEKRIKLESQINQSVLVSSVADVLACGGPRSSQHCGBGS 1139
Db 1085 KTAHRVDIAKYLGGLREQEKRIKLESQINQSVLVSSVADVLACGGPRSSQHCGBGS 1144
QY 1140 QLVAAHRGGLDGEWQFAGAGOPPSDT 1165
Db 1145 QPASARDREYDE-----AGLPHSDT 1164

RESULT 10
AAB86163
ID AAB86163 standard; protein; 872 AA.
XX
AC AAB86163;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human MTR1 protein without exon 18 fragment.
XX
KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW cell growth; cell death; cell differentiation; urogenital disease;
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW rhabdomyosarcoma.
XX
OS Homo sapiens.
XX
FN WO200132693-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-DE003876.
XX
PR 04-NOV-1999; 99DE-01053167.
XX
XX (UYGU-) UNIV GUTENBERG JOHANNES.
PA
PI Prawditt D, Pelletier J, Zabel B;
DR WPI: 2001-316417/33.
DR N-PSDB; AAH20574.
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
PS syndrome and tumors, also related proteins and antibodies.
XX Claim 10; Fig 4; 46pp; German.

This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BWS, Wilms tumor, rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant production of MTR1 proteins (II) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or anti-DNA antibodies. (II) are used to raise Ab, as reagents in competitive assays for (II), as tissue markers; for identifying interacting proteins and in screening for (ant)agonists. This sequence represents a human MTR1 protein described in the method of the invention

SQ Sequence 872 AA;

Query Match 74.4%; Score 4534; DB 4; Length 872;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQDVQGRPGSPGDAEDRRRLGHRGEVNFVGGGKRGKRVVPSPGVAPSLFDLLAEW 60
 DB 1 MQDVQGRPGSPGDAEDRRRLGHRGEVNFVGGGKRGKRVVPSPGVAPSLFDLLAEW 60

QY 61 HLPAPNLVSLVGEEOFPAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLARHYQAV 120
 DB 61 HLPAPNLVSLVGEEOFPAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLARHYQAV 120

QY 121 RDHSLASTSTKVRVAVGMSALGRVLRHRLRILEBAQEDFPVHYPEDDGGSGPLCSLDSNL 180
 DB 121 RDHSLASTSTKVRVAVGMSALGRVLRHRLRILEBAQEDFPVHYPEDDGGSGPLCSLDSNL 180

QY 181 SHFILVEPDPGKGGDLTELRLLEKHI SEORAGYGGTGSIEIPVCLLVNGDPNTLERI 240
 DB 181 SHFILVEPDPGKGGDLTELRLLEKHI SEORAGYGGTGSIEIPVCLLVNGDPNTLERI 240

QY 241 SRAVEQAAPWLLVGGGGIADVLAAALVNQPHLLVPKVAEKQFKEPFSKHFSEDIWRWT 300
 DB 241 SRAVEQAAPWLLVGGGGIADVLAAALVNQPHLLVPKVAEKQFKEPFSKHFSEDIWRWT 300

QY 301 KLLQNTTSHOHLTVYDFQEGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAWDR 360
 DB 301 KLLQNTTSHOHLTVYDFQEGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAWDR 360

QY 361 VDIKSEIENGVEWKSCLDEEVMVDALVSNKPEFVRLFVNDGADVADFTYGRLOELYR 420
 DB 361 VDIKSEIENGVEWKSCLDEEVMVDALVSNKPEFVRLFVNDGADVADFTYGRLOELYR 420

QY 421 SVSRKSLLDLQKQEEARLTLAGTGTOAAREPPAGPAPFSLHVSRLVKFLQDACRG 480
 DB 421 SVSRKSLLDLQKQEEARLTLAGTGTOAAREPPAGPAPFSLHVSRLVKFLQDACRG 480

QY 481 FYQDGRGDRRAEKGPAKRPCTGQKWLDDLNQSENPRDLFLWAVLQNRHMAITYFWAM 540
 DB 481 FYQDGRGDRRAEKGPAKRPCTGQKWLDDLNQSENPRDLFLWAVLQNRHMAITYFWAM 540

QY 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAFALLV 600
 DB 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAFALLV 600

QY 601 RNRCSWKTTLHLATEADAKAFFHDGVOAFLTRIWGDMAGTPILRLGAFICPALV 660
 DB 601 RNRCSWKTTLHLATEADAKAFFHDGVOAFLTRIWGDMAGTPILRLGAFICPALV 660

QY 661 YTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
 DB 661 YTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720

QY 721 LTRWKFVGPVTVFLGNVVMYFAFLFTYVLLVDPRPPGPGSGPEVTLVFWFTLVL 780
 DB 721 LTRWKFVGPVTVFLGNVVMYFAFLFTYVLLVDPRPPGPGSGPEVTLVFWFTLVL 780

QY 781 BEIRQGFTEDETHLVKFTLVVGNWKNKCDMAIFLTVGVTCRMLPSAFEAGRTVLAM 840
 DB 781 BEIRQGFTEDETHLVKFTLVVGNWKNKCDMAIFLTVGVTCRMLPSAFEAGRTVLAM 840

QY 841 DMVFTLRLIHFAIHKQLGPKIIVVERM 869
 DB 841 DMVFTLRLIHFAIHKQLGPKIIVVERM 869

RESULT 11
 ABG61907
 ID ABG61907 standard; protein; 1166 AA.
 XX AC
 XX ABG61907;

DT 15-AUG-2002 (first entry)
 XX Prostate cancer-associated protein #108.
 DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 XX Mammalia.
 OS
 XX W0200230268-A2.
 PN
 XX 18-APR-2002.
 PD
 XX 12-OCT-2001; 2001WO-US032045.
 PF
 XX 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276888P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX
 PI WPI; 2002-471335/50.
 XX N-PSDB; ABK92224.
 DR
 XX Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 27; Page 391; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridise to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABG61800-ABG61944 represent prostate cancer-associated proteins.
 XX
 SQ Sequence 1166 AA;

Query Match 40.2%; Score 2448.5; DB 5; Length 1166;
 Best Local Similarity 45.6%; Pred. No. 9e-223;
 Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVNFVGGGKRGKRVVPSPGVAPSLFDLLAEHLHPAPNLVSLVGEEOFPAMKSWLR 85
 DB 26 GELDTGAGRKSHSLSDRTDPAAYVSLVTRTWGFRAPNLVSVLGGSGPVLQTLQ 87

QY 86 DVLKGLVKAAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGMSALGRV 145
 DB 86 DVLKGLVKAAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGMSALGRV 145

QY 88 DLRRLVRAAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGMSALGRV 146
 DB 88 DLRRLVRAAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGMSALGRV 146

QY 146 LHRRLVRAAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGMSALGRV 200
 DB 146 LHRRLVRAAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGMSALGRV 200

QY 147 RNRDTLNPKGSPFARYWRGDPED--GVQFP---LDVNYSAFFLVDGTHGCLGGERNF 201
 DB 147 RNRDTLNPKGSPFARYWRGDPED--GVQFP---LDVNYSAFFLVDGTHGCLGGERNF 201

201	QY	RURLEKHISEQ	RAGYGGTGS	IFIPVLC	LLVNGD	PNTLERIS	NAVEQA	APWLL	IVSGGIA	260	
202	Db	RURLESYISQ	KTG	GGTG-IDIPV	LLLLIDG	DEKMLTR	ENATQA	QLPCL	LIVAGSGAA	260	
261	QY	DVLAALV	QPHLLVP	-----	KVAEKQ	KEKFP	SKHFSW	EDIV	RWTKL	QNITSHQ	313
261	Db	DCIAET	LIED--	TLAPG	SGAR	GEARD	RIRRRFPK	-----	GDEVL	QAQVERIM	313
314	QY	TVYDFQ	EGSEELDT	VILKAL	VKACKSH	SOEQD	YDLDEL	KLAV	MDRVD	IAKSEIFNG	373
314	Db	TVYSSE	-DGSE	EFETIV	KALVKAC	-GSSE	ASAYL	DEL	LAVAN	NRVDIA	370
374	QY	EWKSCD	LEEVMD	ALVSN	KPEF	VRFLRV	FDNG	ADV	FLTY	GRLOEL	433
371	Db	QWRSF	LEASL	MDALL	NDRPE	FRLLI	ISHGL	FLTP	MR	LAQLY	430
434	QY	RKQEE	ARLTLAGL	-GTQ	QARE	PPAG	PPAP	FLS	HE	SVRLK	491
431	Db	QASH	SAGTK	APAL	KGGA	AEURP	-----	DVGH	VLRL	KKCA	480
492	QY	RAEKG	PAK	PTG	OKW	LIDL	LNQKS	-----	ENP	WRDL	542
481	Db	-----	PQ	GGES	MYLL	SDKAT	SP	SID	AGL	QAP	535
543	QY	EGVA	ALAA	AKKIL	KENSH	LETE	AARAT	REA--	KYER	LALD	600
536	Db	NAVSS	ALGAC	LLR	VMAR	LEP	DEAE	ARRK	DLAF	KFEG	595
601	QY	RNR	CWSKT	TC	LHAT	EADAK	AF	FAHD	GVQAF	TRI	660
596	Db	RRCL	WDGAT	C	LQ	AMQ	ADAR	AF	QDV	OSLIT	655
661	QY	YTN	LITF--	SEE	AP	RTGL	ED	LO	LSL	DTK	712
656	Db	YTRL	ITFR	KSE	EB	PTRE	LE--	EDM	SV	NGE	713
713	QY	--	RC	PR	AV	LLTR	WR	K	FW	AG	770
714	Db	RCG	RRCC--	LR	RF	HF	WG	AP	VTIF	M	768
771	QY	LYF	VV	FT	VL	BE	IR	Q	GF	T	819
769	Db	LYF	WAF	TL	CEL	R	Q	L	S	G	828
820	QY	VG	T	C	R	M	L	P	S	A	879
829	Db	LG	V	C	R	L	T	P	G	L	868
880	QY	LS	V	M	L	V	A	G	V	T	936
889	Db	LG	W	L	V	A	G	V	A	G	948
937	QY	PL	L	L	E	D	S	P	-----	SC	991
949	Db	P	G	F	W	A	H	P	P	G	1008
992	QY	FW	K	Q	R	N	L	I	V	E	1042
1009	Db	Y	W	K	A	Q	R	V	L	I	1068
1043	QY	LP	D	L	O	K	V	T	W	E	1102
1069	Db	-----	AER	K	L	T	W	S	V	H	1124
1103	QY	K	C	L	E	S	Q	I	N	C	1129
1125	Db	K	V	L	E	R	E	V	O	C	1156

RESULT 12
AAAY95436
ID AAAY9
XX

AC		AA9Y5436;			
XX					
DT		10-OCT-2000 (first entry)			
DE					
XX		Human calcium channel SOC-3/CRAC-2.			
XX		SOC-3/CRAC-2; calcium channel; human; store operated channel;			
KW		calcium release activated channel; therapy; diagnosis;			
KW		lymphocyte proliferative disorder.			
RX					
OS		Homo sapiens.			
PV		WO200040614-A2.			
XX					
PD		13-JUL-2000.			
XX					
PF		20-DEC-1999; 99WO-US029996.			
XX					
PR		30-DEC-1998; 98US-0114220P.			
PR		29-JAN-1999; 99US-0120018P.			
PR		22-JUN-1999; 99US-0140415P.			
XX		(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.			
PA					
XX		Scharenberg AM;			
PI					
DR		WPI; 2000-465957/40.			
N-		PSDB; AAA49923.			
XX		New SOC-CRAC calcium channel polynucleotides and polypeptides used to diagnose and treat proliferative disorders associated with the channel, and to screen for novel modulators of the channel. Claim 14; Page 100-103; 108pp; English. The present sequence is that of human SOC-3/CRAC-2, a member of a novel family of store operated channel (SOC) or calcium release activated channel (CRAC) polypeptides that modulate Ca ²⁺ flux into and out of a cell, and which may be activated upon depletion of Ca ²⁺ from intracellular calcium stores, allowing Ca ²⁺ influx into a cell. SOC-3/CRAC-2 is expressed predominantly in colon and kidney. Compositions for expressing functional SOC-CRAC calcium channel polypeptides in cells are expected to be useful for treating patients that have reduced extracellular calcium influx into their SOC-CRAC-expressing cells. They will also be useful for delivering therapeutic and/or imaging agents to such cells to modulate proliferation and growth. SOC-CRAC polypeptides also represent targets for designing and/or identifying inhibitors that block lymphocyte proliferation and binding agents that selectively bind to SOC-CRAC polypeptides to which drugs or toxins can be conjugated for delivery to SOC-CRAC expressing cells. Methods for determining the level of SOC-CRAC expression in a subject can be used to assess the presence, or absence, or stage of a proliferative disorder, e.g. a lymphocyte proliferative disorder			
XX					
SQ		Sequence 1214 AA; Query Match 40.2%; Score 2448.5; DB 3; Length 1214; Best Local Similarity 45.6%; Pred. No. 9.6e-223; Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26; QY 26 GEVNFGSGKKRGKGFVRVPSPGVAHSVLFDDLLAEWHLPAPNLVVSLVGEEQPFAKMWSLR 85 :: :: :: :: :: :: :: :: :: :: :: :: : DB 76 GELDFTAGRKHSNFLRLSDRTDPAAYSVLTVTRTWGFAPNALVVSVLGGSGGPVLTWLQ 135 :: :: :: :: :: :: :: :: :: :: :: : QY 86 DVLKRGLVKQAOSTGANILTSALRVGLRHVGVQAVRDHLSLASTSTKVHVVAWGASLCGRV 145 :: :: :: :: :: :: :: :: :: :: :: : DB 136 DLLRRGLVRAAQSTGANIVTGCGLHTGHGRHHVGAVRDHQMASTG-GTKVMANGVAPGWV 194 :: :: :: :: :: :: :: :: :: :: :: : QY 146 LHRRTLEBAQEDFPVHY-----PEDDGSGSQGPLCSDLNSLNHLFIIVEPCPGKGDLTEL 200 :: :: :: :: :: :: :: :: :: :: :: : DB 195 RNRDTLINPKGSFPPARYWRGDPE--GVQFF---LDYNISAFFLVVDGTGCLCGENRF 249 : :: :: :: :: :: :: :: :: :: :: : QY 201 RLRLFKHTISEQRAGYGTTGSTIEIPVLILLNGDPNTLERISRAVEQAAPNWILLVSGSgia 260			

Db 250 RLRLSYISQKTVGGTG-IDIVLILLIDGDEKMLTRIENATQAOPLCLLVAGSGAA 308
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKPKPKSHFSDIVRWTKLQNTISHQHLL 313
Db 309 DCLAETLED--TLAPSGGARQGEARDIRFFPK-----GDLEVLQAVQVIMTRKELL 361
Qy 314 TVYDFEGSGEELDTVLKALVKACKSHSQBPQDYLDELKLAAMDVRDIAKSEIFNGDV 373
Db 362 TVYSSE-DGSEEFETIVLKVKAC--GSSEASAYLDELRLAVANVRVDIAQSELFRGDI 418
Qy 374 EWKSCDLEEVWVDALVSKNPEFVRLFDVNGADVADFLTYGRLOELYSRVSRLFLDLQ 433
Db 419 QWRSFHLEASLMDALLNDREFVRLLSHGLSGHFTPMRLAQLYSAAPSNLSIRLLD 478
Qy 434 RKQEEARLTLAAGL--GTQOAREPPAGPPAFSLHVSRLVLDKQACRGVQDGRGDR 491
Db 479 QASHSAGTKAPALKGGAELRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH 528
Qy 492 RAEGPAKRPFGQKWLIDLNOKS-----ENPRDLFLWAVLQNRHEMATYFWAMGQ 542
Db 529 -----PQCGFESWYLLSDKATSPSLDAGLQAPWSDLLWALLNRAQWAMYFWMG 583
Qy 543 EGVAALAAACKILKEMSHLETEAFAARATREA--KYERLALDLFSECYNSSEARAFALV 600
Db 584 NAVSSALGACLLURVWARLEPDAEAAARRKDLAFKFGMGVDLFGECYRSEVRAARLL 643
Qy 601 RNRCSWKTCLHLAVTEADAKAFHAGVQAFTRIWWGDMAGTPTLRLIGLFLCPALV 660
Db 644 RRCPLMGDAICLQAWQADARAFQDGVOSLITQKWWGDMASTPTIWLALVAFPCPLI 703
Qy 661 YTNLITP--SEAPLRTGLDLODLSLOTESPLYLQSRVBEELVEAPRAQGD----- 712
Db 704 YTRLITFRKEEPTRELE--FDMDSVINGEVPVGTADPAEKTPLGVPRQSGRPGCGG 761
Qy 713 --RGPAVFLTLTKRWKFWGAPVTFLGNVWYAFILFYLLVLLDFRPPQPSGPEVT 770
Db 762 RCGRRC---LRWFHFWGAPVTIPMGVNVSYLLFLLSRVLVDFQAP--PGSLELL 816
Qy 771 LYFWFVTLVLEIRQGFDTEDT-----HLVKFTLVGNWNNKCDMVALFLPI 819
Db 817 LYFWAFTLLCEELRQGLSGGGSLAGGPGPGHASLSQRULRYLAOSWQCDLVALTCFL 876
Qy 820 VGVTCMLPSAFAGRTVAMDPMFTLRLIHIFAIHKQLGPKIIIVVERMMKDVFFFLFF 879
Db 877 LGVGCRLTGLYHLGRVLCIDPMFTVTRALLHFTVKNQLGPKIVIVSKMKDVFFFLFF 936
Qy 880 LSWLVVAYGVTQALLPHDGRLEWIFRVRVLPYQIIFQIPDLDEIDARV---NCSTH 936
Db 937 LGWLVVAYGATGELRLPRDSDFPSILRRVFRVFPYQIIFQIPQEDMDVALMEHSCSE 996
Qy 937 PLLLEDSP-----SCPSLYANMLVILLVTLVLLVTVNLLMLLIAMFSYTFQVVOGNADM 991
Db 997 PGFWAHPGQAAGTCVSQVANMLVLLLVIFLLVANILLVNLIIAMFSYTFGKVGQNSDL 1056
Qy 992 FWKQRYNLIVYHERPALAPPILLSHLSLTLRRVFKK-----BAEHKREHLERD 1042
Db 1057 YWKAQRYLRIRFHSRPPALAPPFIVISHLRLRLQLCRPRSPQSPSSPALEHFRVLSKE 1116
Qy 1043 LPDPLDQKVVTWETOKENFLSKWEXRDRDSGEVLKRTAHRVDFITAKYLGGLRQEKRI 1102
Db 1117 ----AERKLLTWESVHKNFLARARDKESERLKTTSQKVDLALKQLGHIREVEQRL 1172
Qy 1103 KLESQINVCYSLVSVSADVLAQ-----GGP 1129
Db 1173 KVLREVOQCQSRVLGVVAELRSALLPPGGP 1204

RESULT 13
AAE20283
ID AAE20283 standard; protein; 1214 AA.
XX
AC AAE20283;

XX 18-JUN-2002 (first entry)
DT
XX
DE Human Trp9 protein.
XX
KW Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
KW transient receptor potential; calcium channel protein; Trp8a; Trp8b;
KW molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
KW tumour; chorion carcinoma; lung cancer; antisense therapy.
XX
OS Homo sapiens.
XX
PN WO200210382-A2.
XX
PD 07-FEB-2002.
XX
PF 18-JUL-2001; 2001WO-EP008309.
XX
PR 28-JUL-2000; 2000US-0221513P.
XX
PA (WISS/) WISSENBEACH U.
XX
PI Wissenbach U;
XX
DR WPI; 2002-269013/31.
DR N-PSDB; AAD32372.
XX
PT Novel isolated nucleic acid encoding human prostate carcinoma associated
PT protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
PT useful as molecular markers for diagnosing prostate cancer.
XX
PS Claim 1; Fig 9A; 70pp; English.
XX
CC The invention relates to human prostate carcinoma associated proteins
CC such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and
CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
CC Trp10 are novel calcium channel proteins. Sequences of the invention are
CC useful as molecular markers for diagnosing prostate cancer. Sequences of
CC the invention, their antibodies, inhibitors and antisense molecules are
CC useful for preventing, treating or ameliorating a prostate tumour,
CC endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
CC cancer of the lung or melanoma. Polynucleotides of the invention are used
CC in antisense therapy. The present sequence is human Trp9 protein
XX
SQ Sequence 1214 AA;

Query Match 40.1%; Score 2444.5; DB 5; Length 1214;
Best Local Similarity 45.5%; Pred. No. 2.3e-222;
Matches 533; Conservative 177; Mismatches 351; Indels 111; Gaps 26;

Qy 26 GEVNTGGSGKKGKFRVPSGVAPSVLFDLLLAETHLPAPNLVSLVGEQPPAMKSWLR 85
Db 76 GELDTGTAGRKHNSFLRSLDRTPDAVYSLVTRTWGFRAPNLVSVLGGSGPVLQTLQ 135
Qy 85 DVLRKGLVKAQSTGAWILTSALRYGLARHVGQAVRDHSLASTSTKRVVAVGMASIGRV 145
Db 136 DLLRGLVRAAOSTGAWIVTGLHGTGIGHVGVAVRDHOMASTG-GTKVVAVGVPWGVV 194
Qy 146 LHRRILEAQAQDFPVHY-----PEDDGGSQGPLCSDLSNLSHFILVPEPGPKGDLTEL 200
Db 195 RNRDTLINPKGSFPARYRWGPPED--GVQFP--LDYNSAFFLVDDGTHCLGENRF 249
Qy 201 RLRLKHHISEQAGVGGTGTSTIPVCLLVNGDPNLTLSRISRAVQAPAWLILVSGGTA 260
Db 250 RLRLSYISQKTVGGTG-IDIVLILLIDGDEKMLTRIENATQAOPLCLLVAGSGAA 308
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKPKSHFSDIVRWTKLQNTISHQHLL 313
Db 309 DCLAETLED--TLAPSGGARQGEARDIRFFPK-----GDLEVLQAVQVIMTRKELL 361
Qy 314 TVYDFEGSGEELDTVLKALVKACKSHSQBPQDYLDELKLAAMDVRDIAKSEIFNGDV 373
Db 362 TVYSSE-DGSEEFETIVLKVKAC--GSSEASAYLDELRLAVANVRVDIAQSELFRGDI 418

QY	374	EWKSCDLEEVMDALVSNKPEFVVDNGADVADELTYGRLOELVRSVRKSLDLQ	433
Db	419	QMRSFHLEASMDALLDPEFVLLISHGUSLGHFLTPMDLAQYSAAPNSLRNLLD	478
QY	434	RKQBEARLTLAGL--GTQAREPPAGPAPAFSLHEVSRVLKDFLOQACRGFYQDGRPGDRR	491
Db	479	QASHSAGTKAPALKGAAELRPP-----DVGHVRLMLGKMCAPRYPSGGAMDPH	528
QY	492	RAEKGPAKRTGQKWLLDLQKS-----ENPWRDLFLWVLONRHEMATYFWAQ	542
Db	529	-----PGQFGESMYLLSDKATSPSLDAGLQAPWSDLLWALLNRAQMAFYWENG	583
QY	543	EGVAALAAACKILKEMSHLETEAARATREA--KYERLALDLRSECYNSSEARAFALL	600
Db	584	NAVSSALGACULIRVMARLEDEAEARRKDLAFKFEKGVDLDFEGCYRSSEVRAARLL	643
QY	601	RNRCSWXTTCILHATEADAKAFHAGVQAFLTRIWMGDMAAGTPILRLGAFICPALV	660
Db	644	RRCPLMGDATCLOLAWQADARAFQAQGVQSILITQKMGDMASSTPIWALVLAFCPLI	703
QY	661	YTNLITF--SBEAPLRTGLELDLQDLSLDTKESPLYGLQSRVEELVEAPRAQD-----	712
Db	704	YTRLITFRKSEEPRELE--FMDSVINGEPVGTADPAEKTPLGVPRSGRPGCCGG	761
QY	713	--RGPRAVFLTRMRKFWGAPVTVFLGNVVMYFAFLFVTVLLVDFRPPPOGSGPEVT	770
Db	762	RCGGRRC---LRWFHFGVGPVTFIWMGNVSVLLFLLFSRVLVDFQAP--FGSLELL	816
QY	771	LYFWFTVLVEIRQGFTEDEUT-----HLVKFTLYVGDNNKNCMDVAIFLFI	819
Db	817	LYFWAFTLLCELRQGLSGGSLASGGPGPGHSHLSQRLRLYLADSNQCCLVALTCFL	876
QY	820	VQVTCRMPLPSAEAGRTVLAMDFWFTTLRIHIFAIHKOLGPKIIVVERMKDVEFEFF	879
Db	877	LGVGCRLLTFLGHLGRTVLCIDFMVFTVLLHIFTNKGOLGPKIVIVSKOMKDVFFELF	936
QY	880	LSVLLVAVGVTTOALLHPDHGRLEWFRVLRYPLQIFGQIPDLDEIDEARV---NCSTH	936
Db	937	LGVLVAVGATEGLLRPDSDFPSSILRRVFRPYLQIFGQIPQEDMDVALMEHNSCSSE	996
QY	937	PLLEDSP-----SCPSLYANWLVLVLLVTFLLVNVLMNLLIAMFSYTFQVQGNADM	991
Db	997	PGFWAHPGCAQAGTCVSQYANWLVLVLLVIFLLVANILLVNLIIAMFSYTFQVQGNADL	1056
QY	992	FKHFORNYLIVEYHERPALAPPILLSHLSLTLRRVFKK-----EAEHKREHLERD	1042
Db	1057	YKQAQRYRLIREFHSRPAAPPFIVISHRLRLQLCRRPRSPQSPSPALEHFRVYLSKE	1116
QY	1043	LPDPLDQVVTWETVQKENFLSKWEXRRDSEGEVLRKTAHRVDFITAKYLGGLRQEKRI	1102
Db	1117	-----AERKLLTWESVHKEFNLLARARDKRESDSERLKRITSQKVLALKQLGHIREYEQRL	1172
QY	1103	KCLESGQYCSVLVSSVADVLAQG-----GGP	1129
Db	1173	KVLEREVQCCSRVLGWVAEALSALLPPGGP	1204
RESULT 14			
AA885974	ID	AA885974	standard; protein; 1129 AA.
XX	AC	AA885974;	
XX	AC	AA885974;	
XX	DT	30-NOV-2001	(first entry)
XX	DE	Human TLCC polypeptide.	
XX	DE	Human TLCC polypeptide.	
KW	KW	TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;	
KW	KW	hepatotropic; cardiac; antiarteriosclerotic; antiinflammatory; virucide;	
KW	KW	cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;	
KW	KW	gene therapy.	

OS	XX	Homo sapiens.	
XX	XX	Key	Location/Qualifiers
XX	XX	Peptide	1084..1129
FT	FT		/note= "the residues in this region are not indicated in
FT	FT		the sequence present in the sequence listing, but
FT	FT		indicated in the Figure"
XX	XX	WO200162794-A2.	
XX	XX	30-AUG-2001.	
XX	XX	20-FEB-2001; 2001WO-US005529.	
XX	XX	22-FEB-2000; 2000US-00510706.	
XX	XX	31-MAY-2000; 2000US-00583373.	
XX	XX	08-AUG-2000; 2000US-00634669.	
XX	XX	(MILL-) MILLENNIUM PHARM INC.	
XX	XX	Glucksmann MA, Curtis RAJ, Lora JM;	
XX	XX	WPI; 2001-557700/62.	
XX	XX	N-PSDB; AAH76383, AAH76384.	
XX	XX	New isolated nucleic acid encoding a transient receptor potential-like	
XX	XX	calcium channel for identifying modulators that can be used to treat	
XX	XX	hepatic or cardiovascular disorders.	
XX	XX	Claim 14; Fig 1A-D; 16pp; English.	
XX	XX	The invention provides isolated nucleic acids encoding a human transient	
XX	XX	receptor potential (TRP) family member, called TRP-like calcium channel	
XX	XX	(TLCC) polypeptide. The TLCC polypeptide can be expressed by standard	
XX	XX	recombinant methodology. The TLCC polynucleotides and polypeptide are	
XX	XX	used to identify modulators that can be used to treat a hepatic or a	
XX	XX	cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other	
XX	XX	disorders that can be treated are hepatitis, liver tumors, cirrhosis of	
XX	XX	the liver, hemochromatosis, liver parasite induced disorders, central	
XX	XX	nervous system disorders, pain disorders, or disorders of cellular	
XX	XX	growth, differentiation or migration. The TLCC polynucleotides,	
XX	XX	polypeptide, protein homologs and antibodies to the proteins can be used	
XX	XX	in predictive medicine (e.g. diagnostic assays, prognostic assays,	
XX	XX	monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies	
XX	XX	can isolate TLCC proteins, regulate the bioavailability of TLCC	
XX	XX	proteins, and modulate TLCC activity. The present sequence represents the	
XX	XX	human TLCC polypeptide	
XX	XX	Sequence 1129 AA;	
XX	XX	Query Match	39.6%; Score 2412.5; DB 4; Length 1129;
XX	XX	Best Local Similarity	45.6%; Pred. No. 2.3e-219;
XX	XX	Matches	528; Conservative 174; Mismatches 346; Indels 111; Gaps 26;
QY	39	KFVRVPSGVAPSVLPDILLAEHLPAPNLVSLVSGEEQPFAMKSLRDLVRLKGLVKAQS	98
Db	4	QFLRLSDRTDPAAYSLVTRTWGFRAPNLVSVLGGSGGVPVLTQWLQDLRLGLVRAQS	63
QY	99	TGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMSAGSLGRVLRHRIIEEAQEDF	158
Db	64	TGAWIVTGGLHTGIGHVGVAVRDHQMSTG-GTKVAVGAPVGVVNRDRLINPKGSF	122
QY	159	PVHY-----PEDDGGSGQLCSLDNSLHFLVPEPGPKGGLTELRLRLEKHISEQRA	213
Db	123	PARYRWGDPED--GVQFF---LDVNYSAFFLVDDGTGCLGGENFRRLRLESYSQCKT	177
QY	214	GYGGTGSIEIPVLCLLVNGDPNTLBRISRAVEQAAPLWILVSGSGIADVLAAVLNPHLL	273
Db	178	GVGGTG-IDIPVLLILLIDGEXMLTRIENATQQLPCLLVAGSGGAADCLAELED--TL	234
QY	274	VP-----KVAEKQPKFKFPKHSWEDIVRWTKLLQNTSHQLLTVVDFQSGSEEL	326
Db	235	AFSGGARGQGEARDIRIRFFPK-----GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF	288

18607; calcium signalling; growth; differentiation; capacitative calcium channel; store-operated calcium channel; SOC; plasma membrane; calcium ion; cytosol; modulator; membrane excitability; action potential; excitation; neurite outgrowth; synaptogenesis; signal transduction; angiogenesis; cell proliferation; vascular tone; gene therapy; diagnosis; cardiovascular disorder; atherosclerosis; rheumatoid arthritis; endothelial cell disorder; tumour metastasis; psoriasis; central nervous system disorder; diabetes; hepatic disorder; hepatitis; cirrhosis; Parkinson's disease; multiple sclerosis; epilepsy; cancer; cellular proliferation disorder; migration disorder; therapeutic.

Key Region	Location/Qualifiers
1. .1083	/note= "This region is shown as SEQ ID NO:2 in the sequence listing of the specification, but is only a shorter version of SEQ ID NO:2 shown in Figure 1"

US2002142377-A1.

03-OCT-2002.

20-FEB-2001: 2001US-00789481

22-FEB-2000: 2000US-00510706

31-MAY-2000; 2000US-00583373.
09-AUG-2000; 2000US-00534550

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(CURT//) CURTIS R A J.

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

N-PSDB; ABS58041.

Isolated transient

disorders, pain, c

Claim 14; Fig 1; 80pp; English.

The invention discloses an isolated transient receptor potential (TRP)-like calcium channel (TLCC) polypeptide (186007). Calcium signalling has been implicated in the regulation of a variety of cellular responses, such as growth and differentiation. TLCC is a member of the capacitative calcium channel group or store-operated calcium channel (SOC) which is activated in the plasma membrane to import calcium ions from the extracellular environment to the cytosol. The nucleic acids, polypeptides and antibodies of TLCC are useful for detecting its presence in a sample for identifying a compound which binds to it and identifying a compound which modulates its activity. Modulators of TLCC can be used to modulate membrane excitability, wave forms and frequencies of action potentials, thresholds of excitation, neurite outgrowth and synaptogenesis, signal transduction, angiogenesis, endothelial cell proliferation and vascular tone. The nucleic acid and polypeptide are also useful (using gene therapy) for diagnosing and treating cardiovascular disorders, such as atherosclerosis and restenosis, endothelial cell disorders, such as tumour metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic disorders such as hepatitis and cirrhosis, central nervous system disorders such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and epilepsy, cellular proliferation disorders, such as cancer, and growth, differentiation or migration disorders. TLCC can also be used in predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics) and in methods of treatment (e.g. therapeutic and prophylactic). The sequence presented is the human TLCC, 18607 protein

Sequence 1083 AA;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:06:14 ; Search time 160 Seconds
(without alignments)
2335.021 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence:

1 MODVQGPFGSPGDAEDRRELHRRGEVNFVFGSGKKRGKRVFVPSGVAPSVLFDLLAEW 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6093	100.0	1165	13	US-10-026-188-8
2	6093	100.0	1165	16	US-10-408-765A-1150
3	6057.5	99.4	1164	9	US-09-834-792-5
4	5088.5	83.5	1158	13	US-09-834-792-2
5	5088.5	83.5	1158	13	US-10-026-188-5
6	5008.5	82.2	1165	13	US-10-026-188-2
7	2448.5	40.2	1166	15	US-10-295-027-558
8	2448.5	40.2	1166	15	US-10-295-027-916
9	2448.5	40.2	1214	14	US-10-142-649-2
10	2444.5	40.1	1214	14	US-10-343-114-10
11	2412.5	39.6	1129	9	US-10-391-399-2
12	2353	38.6	1083	5	US-09-789-481C-2
13	2184.5	35.9	1040	16	US-10-312-354-44
14	2039	33.5	1503	12	US-10-369-022-48
15	2039	33.5	1503	12	US-10-405-793-21

16	2039	33.5	1503	13	US-10-007-706-1	Sequence 1, Appli
17	2039	33.5	1503	14	US-10-153-244-104	Sequence 104, App
18	2039	33.5	1503	14	US-10-210-152-21	Sequence 21, Appli
19	2039	33.5	1503	16	US-10-467-163-3	Sequence 3, Appli
20	1619	26.6	678	12	US-10-343-114-8	Sequence 8, Appli
21	1582	26.0	1104	14	US-10-171-319-8	Sequence 8, Appli
22	1567.5	25.7	1104	15	US-10-352-724-1	Sequence 1, Appli
23	1566.5	25.7	1095	9	US-09-759-143-778	Sequence 778, App
24	1566.5	25.7	1095	9	US-09-780-669-778	Sequence 778, App
25	1566.5	25.7	1095	9	US-09-822-827-778	Sequence 778, App
26	1566.5	25.7	1095	9	US-09-895-793-778	Sequence 778, App
27	1566.5	25.7	1095	9	US-09-895-814-778	Sequence 778, App
28	1566.5	25.7	1095	13	US-10-012-896-778	Sequence 778, App
29	1566.5	25.7	1095	14	US-10-205-823-421	Sequence 421, App
30	1566.5	25.7	1095	14	US-10-144-678A-778	Sequence 778, App
31	1566.5	25.7	1095	14	US-10-294-025-778	Sequence 778, App
32	1563.5	25.7	1104	15	US-10-295-027-566	Sequence 566, App
33	1563.5	25.7	1104	16	US-10-408-765A-3018	Sequence 3018, Ap
34	1563.5	25.7	1268	14	US-10-171-319-11	Sequence 11, Appli
35	1558.5	25.6	1095	9	US-09-759-143-780	Sequence 780, App
36	1558.5	25.6	1095	9	US-09-780-669-780	Sequence 780, App
37	1558.5	25.6	1095	9	US-09-822-827-780	Sequence 780, App
38	1558.5	25.6	1095	9	US-09-895-793-780	Sequence 780, App
39	1558.5	25.6	1095	9	US-09-895-814-780	Sequence 780, App
40	1558.5	25.6	1095	13	US-10-012-896-780	Sequence 780, App
41	1558.5	25.6	1095	14	US-10-144-678A-780	Sequence 780, App
42	1558.5	25.6	1095	14	US-10-294-025-780	Sequence 780, App
43	1549.5	25.4	1054	12	US-10-343-114-4	Sequence 4, Appli
44	1545.5	25.4	1104	15	US-10-352-724-3	Sequence 3, Appli
45	1499	24.6	665	16	US-10-763-992-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1

US-10-026-188-8
; Sequence 8, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-1149100S
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ltrpc6
; US-10-026-188-8

Query Match	100.0%;	Score 6093;	DB 13;	Length 1165;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1165;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MODVQGPFGSPGDAEDRRELHRRGEVNFVFGSGKKRGKRVFVPSGVAPSVLFDLLAEW 60		
Db	1	MODVQGPFGSPGDAEDRRELHRRGEVNFVFGSGKKRGKRVFVPSGVAPSVLFDLLAEW 60		
QY	61	HLPAFLVSVLVBGEQPFAMKSWLRLDVLKGLVKAQSTGAWILTSALRVGLARHVQAV 120		
Db	61	HLPAFLVSVLVBGEQPFAMKSWLRLDVLKGLVKAQSTGAWILTSALRVGLARHVQAV 120		
QY	121	RHSLASTSTKRVVAVGVASIGRLVHRRILEEAQDFPVHYPEDDGGSGQLCSLDSNL 180		

Db 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180
QY 181 SHFILVEPPGKGGTGLTELRLLEKHLSEORAGVGGTGSIEIPVLCVLVNGDPTLRI 240
Db 181 SHFILVEPPGKGGTGLTELRLLEKHLSEORAGVGGTGSIEIPVLCVLVNGDPTLRI 240
QY 241 SRVQEAAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKFSPKHSWEDIVRWT 300
Db 241 SRVQEAAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKFSPKHSWEDIVRWT 300
QY 301 KLLQNTSHQHLTVYDFEQSGSELDVILKALVKACKSHSQBPQDYLDELKLA VADR 360
Db 301 KLLQNTSHQHLTVYDFEQSGSELDVILKALVKACKSHSQBPQDYLDELKLA VADR 360
QY 361 VDIKSETFNGDVEWKS CDLEVMVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
Db 361 VDIKSETFNGDVEWKS CDLEVMVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
QY 421 SVSRKSLFLDLLQRKQEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480
Db 421 SVSRKSLFLDLLQRKQEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480
QY 481 FYQDGRPDERRAEKGPAPKPTGQKWLDDLNQSENPRDILFLWAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPDERRAEKGPAPKPTGQKWLDDLNQSENPRDILFLWAVLQNRHEMATYFWAM 540
QY 541 GQEGVAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSSEARAFALLV 600
Db 541 GQEGVAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSSEARAFALLV 600
QY 601 RNRCSWTKTCLHLATEADAKAFFADHGVQAFILTRIMWGDMAAGTPIILLLGAFPCPALV 660
Db 601 RNRCSWTKTCLHLATEADAKAFFADHGVQAFILTRIMWGDMAAGTPIILLLGAFPCPALV 660
QY 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVAPRAQDGRGPRAVFL 720
Db 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVAPRAQDGRGPRAVFL 720
QY 721 LTRWRKFGAPVTFLGNVMVYFAFLFTVYVLLVDPRPPQPGSGPEVTLYFWFTVLV 780
Db 721 LTRWRKFGAPVTFLGNVMVYFAFLFTVYVLLVDPRPPQPGSGPEVTLYFWFTVLV 780
QY 781 EBIROGFTDEDTHLVKXFTLYVGNWNKCDMVAIFLFTVGTCTRMPLSAFEAGRTVLAM 840
Db 781 EBIROGFTDEDTHLVKXFTLYVGNWNKCDMVAIFLFTVGTCTRMPLSAFEAGRTVLAM 840
QY 841 DPMWFTLRLIHFALHKGQPKIIIVVERMKDVFLLFPLSVMLVAYGVTTQALLHPHDG 900
Db 841 DPMWFTLRLIHFALHKGQPKIIIVVERMKDVFLLFPLSVMLVAYGVTTQALLHPHDG 900
QY 901 RLEWIFRVRVLYRPIQIFQOIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVLILV 960
Db 901 RLEWIFRVRVLYRPIQIFQOIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVLILV 960
QY 961 TELLVTNLLNLLIAMSFTYFQVVGQADMFVKFQRYNLI VEHHERPALAPPFILLSHL 1020
Db 961 TELLVTNLLNLLIAMSFTYFQVVGQADMFVKFQRYNLI VEHHERPALAPPFILLSHL 1020
QY 1021 SUTLRVRVKEAEHREHLERDLPDLDQKVTWTQKENTFLSKWEXRRRSEGEVLK 1080
Db 1021 SUTLRVRVKEAEHREHLERDLPDLDQKVTWTQKENTFLSKWEXRRRSEGEVLK 1080
QY 1081 TAHRVDFTAHYGLGRBOEKRIKLESQINYSVLVSSVADVLAQGGPRSSQHCQGSQ 1140
Db 1081 TAHRVDFTAHYGLGRBOEKRIKLESQINYSVLVSSVADVLAQGGPRSSQHCQGSQ 1140
QY 1141 LVAADHRGCLDGWEQAGQPPSDT 1165
Db 1141 LVAADHRGCLDGWEQAGQPPSDT 1165

RESULT 2

US-10-408-765A-1150
; Sequence 1150, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Boon D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1150
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1150

Query Match 100.0%; Score 6093; DB 16; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDVQGPSPGDAEDRRLGLHRGEVNFQSGGKRGKRVFVPSGVAPSVLFDLLLAEM 60
Db 1 MCDVQGPSPGDAEDRRLGLHRGEVNFQSGGKRGKRVFVPSGVAPSVLFDLLLAEM 60
QY 61 HLPAPNLVSVLVEEQEPFAMKSWLRDLVLRKGLVXAAQSTGAWILTSALRVGLARHVGQAV 120
Db 61 HLPAPNLVSVLVEEQEPFAMKSWLRDLVLRKGLVXAAQSTGAWILTSALRVGLARHVGQAV 120
QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180
Db 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180
QY 181 SHFILVEPPGKGGTGLTELRLLEKHLSEORAGVGGTGSIEIPVLCVLVNGDPTLRI 240
Db 181 SHFILVEPPGKGGTGLTELRLLEKHLSEORAGVGGTGSIEIPVLCVLVNGDPTLRI 240
QY 241 SRVQEAAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKFSPKHSWEDIVRWT 300
Db 241 SRVQEAAPWLLVSGGGIADVLALVNQPHLLVPKVAEKQKFKFSPKHSWEDIVRWT 300
QY 301 KLLQNTSHQHLTVYDFEQSGSELDVILKALVKACKSHSQBPQDYLDELKLA VADR 360
Db 301 KLLQNTSHQHLTVYDFEQSGSELDVILKALVKACKSHSQBPQDYLDELKLA VADR 360
QY 361 VDIKSETFNGDVEWKS CDLEVMVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
Db 361 VDIKSETFNGDVEWKS CDLEVMVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
QY 421 SVSRKSLFLDLLQRKQEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480
Db 421 SVSRKSLFLDLLQRKQEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480
QY 481 FYQDGRPDERRAEKGPAPKPTGQKWLDDLNQSENPRDILFLWAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPDERRAEKGPAPKPTGQKWLDDLNQSENPRDILFLWAVLQNRHEMATYFWAM 540
QY 541 GQEGVAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSSEARAFALLV 600
Db 541 GQEGVAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSSEARAFALLV 600
QY 601 RNRCSWTKTCLHLATEADAKAFFADHGVQAFILTRIMWGDMAAGTPIILLLGAFPCPALV 660
Db 601 RNRCSWTKTCLHLATEADAKAFFADHGVQAFILTRIMWGDMAAGTPIILLLGAFPCPALV 660
QY 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVAPRAQDGRGPRAVFL 720

Db 661 YTNLTITFSEAPRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQCDRGPRAVFL 720
QY 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGPEVTLYFWVFTVL 780
Db 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGPEVTLYFWVFTVL 780
QY 781 EEIROGFFTDDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFAEAGRTVLAM 840
Db 781 EEIROGFFTDDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFAEAGRTVLAM 840
QY 841 DMVFTLRILHIHFAIHKQLGPKIIIVVERMKOVFFFLFSLVWLVAAYGVTTOALLHPHDG 900
Db 841 DMVFTLRILHIHFAIHKQLGPKIIIVVERMKOVFFFLFSLVWLVAAYGVTTOALLHPHDG 900
QY 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
Db 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
QY 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFFILLSHL 1020
Db 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFFILLSHL 1020
QY 1021 SLTLRVFVKEAEHKEHLEERDLDPDLDQKVVTWETVQENFLSKWEXRRRDEGEVLRK 1080
Db 1021 SLTLRVFVKEAEHKEHLEERDLDPDLDQKVVTWETVQENFLSKWEXRRRDEGEVLRK 1080
QY 1081 TAHRVDFIAKYLGLREQEKRICKLESQINCSVLVSSVADVLAQGGPRSSQHCGEQSQ 1140
Db 1081 TAHRVDFIAKYLGLREQEKRICKLESQINCSVLVSSVADVLAQGGPRSSQHCGEQSQ 1140
QY 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165

RESULT 3

US-09-834-792-5
; Sequence 5, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:

; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; FILE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165.0589
; CURRENT APPLICATION NUMBER: US/09/834,792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

; LENGTH: 1164
; TYPE: PRT
; ORGANISM: Human
US-09-834-792-5

Query Match 99.4%; Score 6057.5; DB 9; Length 1164;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1161; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MODVQGPSPGDAEDRRELGLHRGEVNFVGGSGKKRGKRVFVPSGVAPSVLFDLLLAEW 60
Db 1 MODVQGPSPGDAEDRRELGLHRGEVNFVGGSGKKRGKRVFVPSGVAPSVLFDLLLAEW 60
QY 61 HLPAPNLVSVLGEQPFAMKSWLRDVLKGLVKAQSTGAMILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSVLGEQPFAMKSWLRDVLKGLVKAQSTGAMILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKRVVAVGMASIGRVLHRRILEAQEDFPVHPEDDGGSGQPLCSLDSNL 180
Db 121 RDHSLASTSTKRVVAVGMASIGRVLHRRILEAQEDFPVHPEDDGGSGQPLCSLDSNL 180

RESULT 4

US-09-834-792-2
; Sequence 2, Application US/09834792
; Patent No. US20020037515A1

QY 181 SHFILVEPFPKGGDGLTELRLLEKHISEORAGYGGTGSIEIPVLCILVNGDPNTLIERI 240
Db 181 SHFILVEPFPKGGDGLTELRLLEKHISEORAGYGGTGSIEIPVLCILVNGDPNTLIERI 240
QY 241 SRAVEQAAPWLILVSGGGIADVLAALVNPQPHLLVPKVAEKQFKEKFPKSHFSMEDIVRWT 300
Db 241 SRAVEQAAPWLILVSGGGIADVLAALVNPQPHLLVPKVAEKQFKEKFPKSHFSMEDIVRWT 300
QY 301 KLLQNTITSHOHLITVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYDELKLAWADR 360
Db 301 KLLQNTITSHOHLITVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYDELKLAWADR 360
QY 361 VDIKSEIEFNGDVEMKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420
Db 361 VDIKSEIEFNGDVEMKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420
QY 421 SVSRKSLLDLQKQEEARLTLAGLGTQOAREPPAGPPAFSLHEYSRVRLKDFLODACRG 480
Db 421 SVSRKSLLDLQKQEEARLTLAGLGTQOAREPPAGPPAFSLHEYSRVRLKDFLODACRG 480
QY 481 FYODGPGRRRAEKGPAKPTGOKWLLDINOKSENPNWDLFLWAVLQNRHEMATTFWAM 540
Db 481 FYODGPGRRRAEKGPAKPTGOKWLLDINOKSENPNWDLFLWAVLQNRHEMATTFWAM 540
QY 541 GQGVAAAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYSNSRARAFALLV 600
Db 541 GQGVAAAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYSNSRARAFALLV 600
QY 601 RNRRCWSKTTCLHLATEADAKAFFAHGQVQAFELTRIMWGDMAAGTPIRLLLGAFCLPALV 660
Db 601 RNRRCWSKTTCLHLATEADAKAFFAHGQV-AFLTRIMWGDMAAGTPIRLLLGAFCLPALV 660
QY 661 YTNLTITFSEAPRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQCDRGPRAVFL 720
Db 661 YTNLTITFSEAPRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQCDRGPRAVFL 720
QY 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGPEVTLYFWVFTVL 780
Db 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGPEVTLYFWVFTVL 780
QY 781 EEIROGFFTDDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFAEAGRTVLAM 840
Db 781 EEIROGFFTDDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFAEAGRTVLAM 840
QY 841 DMVFTLRILHIHFAIHKQLGPKIIIVVERMKOVFFFLFSLVWLVAAYGVTTOALLHPHDG 900
Db 841 DMVFTLRILHIHFAIHKQLGPKIIIVVERMKOVFFFLFSLVWLVAAYGVTTOALLHPHDG 900
QY 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
Db 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
QY 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFFILLSHL 1020
Db 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFFILLSHL 1020
QY 1021 SLTLRVFVKEAEHKEHLEERDLDPDLDQKVVTWETVQENFLSKWEXRRRDEGEVLRK 1080
Db 1021 SLTLRVFVKEAEHKEHLEERDLDPDLDQKVVTWETVQENFLSKWEXRRRDEGEVLRK 1080
QY 1081 TAHRVDFIAKYLGLREQEKRICKLESQINCSVLVSSVADVLAQGGPRSSQHCGEQSQ 1140
Db 1081 TAHRVDFIAKYLGLREQEKRICKLESQINCSVLVSSVADVLAQGGPRSSQHCGEQSQ 1140
QY 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165

GENERAL INFORMATION:
; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; TITLE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165.0589
; CURRENT APPLICATION NUMBER: US/09/834,792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Murine TRP8
US-09-834-792-2

Query Match 83.5%; Score 5088.5; DB 9; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MQDVQGPFGSGDAEDRELGHRGEVNFSGGKGRKFKVPSGVAPSVLFDLLAEW 60
DB 1 MQTQSSCGSPDPDTEGDWEPILCRGEINFGSGKGRKFKVPSGVAPSVLFDLLAEW 60
QY 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCLSDS 178
DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCLSDS 178
QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCLSDS 178
DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCLSDS 178
QY 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPIVCLLVNGDPNLT 237
DB 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPIVCLLVNGDPNLT 237
QY 181 NLSHFILVESGALSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVCLLVNGDPNLT 240
DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVCLLVNGDPNLT 240
QY 238 ERISRAVQAAPWLLVSGGGTADVIAALVNPQLLVPKVAEKQFKFPKPSKHFSWEDIV 297
DB 241 ERISRAVQAAPWLLVSGGGTADVIAALVNPQLLVPKVAEKQFKFPKPSKHFSWEDIV 297
QY 298 RWTKLQNTSHOHLTVYDFEQQSGBELTVILKALVKACKSHQSEQDYDELKJLAVA 357
DB 301 HWTLLQNTIAHPHLLTVYDFEQQSGBELTVILKALVKACKSHQSEQDYDELKJLAVA 360
QY 358 WDRVDIAKSEIPNGDVENKSCDLEVMVDALVSNKPEFVRLPVDNGADVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIPNGDVENKSCDLEVMVDALVSNKPEFVRLPVDNGADVADFLTYGRLOE 420
QY 418 LYRSVRSKSLFDLLQKQEEARLTLAGLTQQAAREPPAGPPAFSLHESVRLKDFLODA 477
DB 421 LYHSVSPKSLFELLQKXHEEGRLLTAGLGAQAARELPGLPAPSLHESVRLKDFLODA 480
QY 478 CRGFTVODRPGDRRAEKGPAKPTGOKWLLDLNOKSENPRDLFLWVLQNRHEMATYF 537
DB 481 CRGFTVODRPGDRRAEKGPAKPTGOKWLLDLNOKSENPRDLFLWVLQNRHEMATYF 536
QY 538 WAMGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAPA 597
DB 537 WAMGREGVAAALAAACKILKEMSHLEKEAEVARTMEAKYEQALADLFSECYNSSEARAPA 596
QY 598 LLVRRNRCSKTTCLHLATEADAKFAFHGDGVQAFTRIWWGDMAGTPIRLKLAGFLCP 657
DB 597 LLVRRNRCSKTTCLHLATEADAKFAFHGDGVQAFTRIWWGDMAGTPIRLKLAGFLCP 656
QY 658 ALVYNTNLTFFSEAPLRTGLELDLQDLSLDTESKPLYGLOKSRVEELVEAPRAQGGPEA 717
DB 657 ALVYNTNLTFFSEAPLRTGLELDLQDLSLDTESKPLYGLOKSRVEELVEAPRAQGGPEA 716
QY 718 VELLTRWRKFWGAPVTVFLGNVMVYFAFLFTYVLLVDFRPPPPQSPGSEVTLVFWVFT 777
DB 717 AELLTRWRKFWGAPVTVFLGNVMVYFAFLFTYVLLVDFRPPPPQSPGSEVTLVFWVFT 776

QY 778 LVLEEIRQGFTEBDETHLVKKFTLYVCDNWNKCDMVAIFLFIYGVTCMLPSAFEAGRTV 837
DB 777 LVLEEIRQGFTEBDETHLVKKFTLYVEDNWNKCDMVAIFLFIYGVTCRMVPSVFEAGRTV 836
QY 838 LAMDEWVFTLRLIHFPAHKQKGLIIVVERMKDVFFFLFFLSVWLVAIVGVTTQALJHP 897
DB 837 LAIDFWVFTLRLIHFPAHKQKGLIIVVERMKDVFFFLFFLSVWLVAIVGVTTQALJHP 896
QY 898 HDGRLEWIFRRVLYRYPYLIQIFGQIPLEIDEARVNCSTHPLLEDSPCSLYANWLVIL 957
DB 897 HDGRLEWIFRRVLYRYPYLIQIFGQIPLEIDEARVNCSTHPLLEDSPCSLYANWLVIL 956
QY 958 LLVFTLLVTVNLLMNLIIAMFSYTFVQVGNADMFQKFORNLIVEYHERPALAPPFLL 1017
DB 957 LLVFTLLVTVNLLMNLIIAMFSYTFVQVGNADMFQKFORNLIVEYHERPALAPPFLL 1016
QY 1018 SHLSLTLLRRVFKKAEHRLERDLDPDLDQKVVTWETVQENFLSKMERKRRDSEGEV 1077
DB 1017 SHLSLTLLRRVFKKAEHRLERDLDPDLDQKVVTWETVQENFLSKMERKRRDSEGEV 1076
QY 1078 LRKTAHRVDFTAKYLGGLRQEKRIKLESQINVCYSLVSSVADVLAQGGGPRSSQHCE 1137
DB 1077 LRKTAHRVDFTAKYLGGLRQEKRIKLESQINVCYSLVSSVADVLAQGGGPRSSQHCE 1136
QY 1138 GSQVLAADHRCGLDQWEPQAGQPPSDT 1165
DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 5
US-10-026-188-5
; Sequence 5, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence
US-10-026-188-5

Query Match 83.5%; Score 5088.5; DB 13; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MQDVQGPFGSGDAEDRELGHRGEVNFSGGKGRKFKVPSGVAPSVLFDLLAEW 60
DB 1 MQTQSSCGSPDPDTEGDWEPILCRGEINFGSGKGRKFKVPSGVAPSVLFDLLAEW 60
QY 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCLSDS 178
DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHPEDDGGSGGGLCLSDS 178
QY 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPIVCLLVNGDPNLT 237
DB 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPIVCLLVNGDPNLT 237
QY 181 NLSHFILVESGALSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVCLLVNGDPNLT 240
DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVCLLVNGDPNLT 240
QY 238 ERISRAVQAAPWLLVSGGGTADVIAALVNPQLLVPKVAEKQFKFPKPSKHFSWEDIV 297
DB 241 ERISRAVQAAPWLLVSGGGTADVIAALVNPQLLVPKVAEKQFKFPKPSKHFSWEDIV 297
QY 298 RWTKLQNTSHOHLTVYDFEQQSGBELTVILKALVKACKSHQSEQDYDELKJLAVA 357
DB 301 HWTLLQNTIAHPHLLTVYDFEQQSGBELTVILKALVKACKSHQSEQDYDELKJLAVA 360
QY 358 WDRVDIAKSEIPNGDVENKSCDLEVMVDALVSNKPEFVRLPVDNGADVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIPNGDVENKSCDLEVMVDALVSNKPEFVRLPVDNGADVADFLTYGRLOE 420
QY 418 LYRSVRSKSLFDLLQKQEEARLTLAGLTQQAAREPPAGPPAFSLHESVRLKDFLODA 477
DB 421 LYHSVSPKSLFELLQKXHEEGRLLTAGLGAQAARELPGLPAPSLHESVRLKDFLODA 480
QY 478 CRGFTVODRPGDRRAEKGPAKPTGOKWLLDLNOKSENPRDLFLWVLQNRHEMATYF 537
DB 481 CRGFTVODRPGDRRAEKGPAKPTGOKWLLDLNOKSENPRDLFLWVLQNRHEMATYF 536
QY 538 WAMGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAPA 597
DB 537 WAMGREGVAAALAAACKILKEMSHLEKEAEVARTMEAKYEQALADLFSECYNSSEARAPA 596
QY 598 LLVRRNRCSKTTCLHLATEADAKFAFHGDGVQAFTRIWWGDMAGTPIRLKLAGFLCP 657
DB 597 LLVRRNRCSKTTCLHLATEADAKFAFHGDGVQAFTRIWWGDMAGTPIRLKLAGFLCP 656
QY 658 ALVYNTNLTFFSEAPLRTGLELDLQDLSLDTESKPLYGLOKSRVEELVEAPRAQGGPEA 717
DB 657 ALVYNTNLTFFSEAPLRTGLELDLQDLSLDTESKPLYGLOKSRVEELVEAPRAQGGPEA 716
QY 718 VELLTRWRKFWGAPVTVFLGNVMVYFAFLFTYVLLVDFRPPPPQSPGSEVTLVFWVFT 777
DB 717 AELLTRWRKFWGAPVTVFLGNVMVYFAFLFTYVLLVDFRPPPPQSPGSEVTLVFWVFT 776

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QY 238 ERISRAVEQAAPMLILVSGGIIADVLAAALVNQPHLLVPKVAEQKFKPKSPKHSFSDIV 297
Db 241 ERISRAVEQAAPMLILVSGGIIADVLAAALVNQPHLLVPKVAEQKFKPKSPKHSFSDIV 300
QY 298 RWTYKLLQNIYSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 357
Db 301 HWTLLQNIYSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 360
QY 358 WDRVDIAKSIIFNGDVEWKSCLDEEVNMDALVSNKPEFVFLFVNDGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSIIFNGDVEWKSCLDEEVNMDALVSNKPEFVFLFVNDGADVADFLTYGRLOE 420
QY 418 LYRSVSRKSLFLLQRLQKQEBEALTLTLAGLCTQQAEPAPGPPAFSLHEVSRLVKDFLODA 477
Db 421 LYHSVSPKSLFLLQRLQKQEBEALTLTLAGLCTQQAEPAPGPPAFSLHEVSRLVKDFLODA 480
QY 478 CRGFYQDGRGDRRAEAKPAKPTGQKWLDDNOKSENPRDLFLWAVLQNRHEMATYF 537
Db 481 CRGFYQDGRGDRRAEAKPAKPTGQKWLDDNOKSENPRDLFLWAVLQNRHEMATYF 536
QY 538 WAMQOEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAF 597
Db 537 WAMRGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAF 596
QY 598 LLVRRNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLP 657
Db 597 LLVRRNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLP 656
QY 658 ALVYTNLITFSEAPRTGLEDLQDLSLDEKSPKYLQSRVVEELVEAPRAQDGRGPA 717
Db 657 ALVYTNLITFSEAPRTGLEDLQDLSLDEKSPKYLQSRVVEELVEAPRAQDGRGPA 716
QY 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFLEYVLLVDRPPPPQSGSEVTLTYFWVFT 777
Db 717 APLTRWRKFWGAPVTVFLGNVVMYFAFLFLEYVLLVDRPPPPQSGSEVTLTYFWVFT 776
QY 778 LVLEIRQGFDTDETHLVKKFTLYVGDNWNKCDMAIFLFIYGVTCRMLPSAFAGRTV 837
Db 777 LVLEIRQGFDTDETHLVKKFTLYVGDNWNKCDMAIFLFIYGVTCRMLPSAFAGRTV 836
QY 838 LAMDFMVFTRLIHIFAIHQKLGPKIIIVERMMKOVFFFLFSLVWMLVAYVTTQALLHP 897
Db 837 LAMDFMVFTRLIHIFAIHQKLGPKIIIVERMMKOVFFFLFSLVWMLVAYVTTQALLHP 896
QY 898 HGRLEWIFRRLVYRVLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANLVL 957
Db 897 HGRLEWIFRRLVYRVLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANLVL 956
QY 958 LLVTFLLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIYVHERPALAPPFILL 1017
Db 957 LLVTFLLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIYVHERPALAPPFILL 1016
QY 1018 SHLSLTLRVFVKEAHEKHEHLERDLPDLDQKVTWETVOKENFLSKMEKRRRDEGEV 1077
Db 1017 SHLSLTLRVFVKEAHEKHEHLERDLPDLDQKVTWETVOKENFLSKMEKRRRDEGEV 1076
QY 1078 LRKTAHRVDIAKYLGLGRLQEKRIKCLRSOINVCVSLVSSVADVLAQGGPRSSOHCE 1137
Db 1077 LRKTAHRVDIAKYLGLGRLQEKRIKCLRSOINVCVSLVSSVADVLAQGGPRSSOHCE 1136
QY 1138 GSQVAAADHRGGIDGWEQPCAGQPPSDT 1165
Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158
```

RESULT 6

US-10-026-188-2

; Sequence 2, Application US/10026188
; Publication No. US20020164645A1

; GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Zhang, Yifeng

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat L-TRP taste predicted protein
US-10-026-188-2

Query Match 82.2%; Score 5008.5; DB 13; Length 1165;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 965; Conservative 77; Mismatches 113; Indels 11; Gaps 3;

QY 1 MDVQPRPGSPGDADREELGLHRGEVNFVGGSGKKRGKRVFVPSGVAPSVLFDLLAEW 60
Db 9 MPMAQSCSPGPPDTGDGWEPLCKGEVNFVGGSGKKRKVKVPSNVAPSMLELLLEW 68
QY 61 HLPAPNLVSLVCEBOPFAMKSWLRDVLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db 69 HLPAPNLVSLVCEBOPFAMKSWLRDVLKGLVKAQSTGAWILTSALRVGLARHVQAV 128
QY 121 RHSLASTSTKVRVAVAGMASLGRVLRILIEAQEDFPVHYDEDDGSGGCLDLSNL 180
Db 129 RHSLASTSTKVRVAVAGMASLGRVLRILIEAQEDFPVHYDEDDGSGGCLDLSNL 188
QY 181 SHFVPEPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPVCLLVNDGPTLER 239
Db 189 SHFVPEPPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPVCLLVNDGPTLER 248
QY 240 ISRAVEQAAPMLILVSGGIIADVLAAALVNQPHLLVPKVAEQKFKPKSPKHSFSDIV 299
Db 249 MSRAVEQAAPMLILVSGGIIADVLAAALVNQPHLLVPKVAEQKFKPKSPKHSFSDIV 308
QY 300 TKLLQNIYSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 359
Db 309 TKLLQNIYSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 368
QY 360 RVDIAKSIIFNGDVEWKSCLDEEVNMDALVSNKPEFVFLFVNDGADVADFLTYGRLOE 419
Db 369 RVDIAKSIIFNGDVEWKSCLDEEVNMDALVSNKPEFVFLFVNDGADVADFLTYGRLOE 428
QY 420 RSVSRKSLFLLQRLQKQEBEALTLTLAGLCTQQAEPAPGPPAFSLHEVSRLVKDFLODA 479
Db 429 RSVSRKSLFLLQRLQKQEBEALTLTLAGLCTQQAEPAPGPPAFSLHEVSRLVKDFLODA 488
QY 480 GFYQDGRGDRRAEAKPAKPTGQKWLDDNOKSENPRDLFLWAVLQNRHEMATYF 539
Db 489 GFYQDGRGDRRAEAKPAKPTGQKWLDDNOKSENPRDLFLWAVLQNRHEMATYF 544
QY 540 MGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAF 599
Db 545 MGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAF 604
QY 600 VRRNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLP 659
Db 605 VRRNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLP 664
QY 660 VYTNLITFSEAPRTGLEDLQDLSLDEKSPKYLQSRVVEELVEAPRAQDGRGPA 719
Db 665 VYTNLITFSEAPRTGLEDLQDLSLDEKSPKYLQSRVVEELVEAPRAQDGRGPA 724
QY 720 LLTRWRKFWGAPVTVFLGNVVMYFAFLFLEYVLLVDRPPPPQSGSEVTLTYFWVFT 779
Db 725 LLTRWRKFWGAPVTVFLGNVVMYFAFLFLEYVLLVDRPPPPQSGSEVTLTYFWVFT 784

QY 780 LEEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLA 839
D5 785 LEEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLA 844
QY 840 MDMVFVTLRLIHI FAIHKQLGPKIIIVVERMMKOVFFFLFSLVNLVAYGVTTQALLHPHD 899
D5 845 IDFWVFTLRLIHI FAIHKQLGPKIIIVVERMMKOVFFFLFSLVNLVAYGVTTQALLHPHD 904
QY 900 GRLEWIFRVLRYPLQIFQOIPLEIDEARVNCSTHLLLEDSPSCPSLYANMLVILL 959
D5 905 GRLEWIFRVLRYPLQIFQOIPLEIDEARVNCSTHLLLEDSPSCPSLYANMLVILL 964
QY 960 VTELLVNTVLLNMLLIAMFSTFQVQGNADMFWKFORYNLIVYHERPALAPFILLSH 1019
D5 965 VTELLVNTVLLNMLLIAMFSTFQVQGNADMFWKFORYNLIVYHERPALAPFILLSH 1024
QY 1020 LSLTLRRVFKAEAKHREHLERDLPDLDQKVVTWETVOKNFSLKMKRRDRDSEGEVLR 1079
D5 1025 LSLVLKQVFEAKHQHLERLDPDPVDQKIITWETVOKNFSLKMKRRDRDSEGEVLR 1084
QY 1080 KTAHRVDIAKYGLREORERIKLESQINVCVSVLSSVADVLAAQGGGPRSSQHCGBGS 1139
D5 1085 KTAHRVDIAKYGLREORERIKLESQINVCVSVLSSVADVLAAQGGGPRSSQHCGBGS 1144
QY 1140 QLVAAHRRGGGLDGEQPGAGOPPSDT 1165
D5 1145 QPASARDREYLE-----AGLPHSDT 1164

RESULT 7
US-10-295-027-558
; Sequence 558, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 558
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-558

Query Match 40.2%; Score 2448.5; DB 15; Length 1166;
Best Local Similarity 45.6%; Pred. No. 6.1e-217;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVNFSGSKRGKGFVPSGVAPSLVDFDILLAEHLPAFLVSLVGEQPFAMKWLRL 85
D5 28 GELDTGAGRKHSNLRSLRSDTDAVYSLVTRTWGFRAPNLVSVLGGSGPVLQWLO 87
QY 86 DVLKGLVAKAAQSTGAMILTSALRVGLARHVQAVRDHSLASTSTKVRVAVAGMASGRV 145
D5 88 DLLRGLVRAAQSTGAMIVTGLHTGIGRHVGVAVRDHMASTG-GTKVAVAGVAPGWV 146
QY 146 LHRRIEAAQDDFPVHY-----PEDDGSQGPLCSLSDNSLSHFLVVEPPGPKDGLTEL 200
D5 147 RNRDTLNPKGSPFARYRWGRDPED--GVQFPF---LDYNSAFVLVDGTHGCLGGRNF 201
QY 201 RLREKHISEORAGVGTGTSTIEIPVLCILVNGDPTNLERISRAVEQAAPWLILVSGSGIA 260
D5 202 RLRLSYISQQTGVGTGTG-IDIPVLLILLIDGDEKMLTRIENATQAQLPCLLVAGSGGAA 260
QY 261 DVLAALVNQPHLLVP-----KVAEKQFKFKPSKHSWEDIVRWTKLLQNLITSHQHL 313
D5 261 DCLAEITLED--TLAPGSGGARQGEARDIRRRFPK-----GDLEVLQAQVERIMTRKELL 313
QY 314 TVYDFEQGSGSELDTVILKALVKACKSHSQSPQDYLDELKLAADVDRVDIAKSEIFNGDV 373
D5 314 TVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYLDELRLAVANRVDIAQSEIFRGDI 370
QY 374 EWKSCDLEVMVDALVSNKPFVRLFDVNGADVADFLTYGRLOELYSRVSRLDFDLIQ 433
D5 371 QWRSFHLERASLMDALNDRPFVRLILSHGLSHGLFTPLMLAQLIYSAAPSNSLRNLDD 430
QY 434 RKQEEARLTLAGL--GTQOAREPPAGPPAFSLHSEVSRVLKDFQDACRGFYODGRPRDR 491
D5 431 QASHSAGTKAPALKGAAELRPP-----DVGHVRLMLLGMKCAPRYPSGGAWDPH 480
QY 492 RAEKGPAPKPTGQKWLILLNQS-----ENPWRDLFLWVLONHEMATYFWAMQO 542
D5 481 -----PGQFGESMYLLSDKATSPSLDAGLQAPWSLWALLNRAQMANIYFEMGS 535
QY 543 EGVAALAAACKILKEMSHLETEAARATREA--KYERLALDLFSECYSNSRARAFAIIV 600
D5 536 NAVSALGACILLRVMALEPDAEAEARKKOLAFKFGGVDFLFGECYRSSEVRAARULL 595
QY 601 RNRCSKTTICILHLATEADAKAFFAHGQVQAFITRWGDMAGTPTILRLGAFICPALV 660
D5 596 RRCPLWGDATCLQAWQADARAFQAQDGVQSLLTKWGMGMASSTTPIWALVAFPCPLI 655
QY 661 YTNLITF--SEAPARTGLELDLSDLTESPLVGLQSRVEELVEAPRAQD----- 712
D5 656 YTRLITFRKSEEPTEELE--FDWDSVINGEPVGTADPAEKTPLGVPRGRCGCCGG 713
QY 713 --RGPRAVFLLTRMKFWGAPVTVFLGNVMVFAFLFVLLVDFRPPPGPSGPEVT 770
D5 714 RCGGRCC---LRWFFHFWGAPVTIEMGNVSVLLFLLFSLRVLLVDFQFAP--PGSLELL 768
QY 771 LYFWVFTLVLEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLA 839
D5 769 LYFWAFTLLCEBLRQGLSGGGSLASGGGPGGHASLSQRRLYLADSNWQCCLVALTCFL 828
QY 820 VGVTCMLPSAFEAGRTVLAIDFMVFTLRLIHI FAIHKQLGPKIIIVVERMMKOVFFFLF 879
D5 829 LGVGCRLTPEGLYHLGRTVLCIDFMVFTLRLIHI FAIHKQLGPKIIIVVERMMKOVFFFLF 888
QY 880 LSVNLVAVGVTTQALLHPHDGRLEWIFRVLRYPLQIFQOIPLEIDEARVNCSTHLLLEDSPSCPSLYANMLVILL 959
D5 889 LGVNLVAVGVATEGLLRFRDSDFPSTLRVFRVPLVQIFQOIPQEDMDVALMEHNSCSSE 948


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QY 1103 KLESQINCVSVSVADVLAAQ-----GGP 1129
Db 1125 KVLREYQCCSRVLGWAEALSRSALLPPGGP 1156

RESULT 9
US-10-142-649-2
; Sequence 2, Application US/10142649
; Publication No. US20030143557A1
; GENERAL INFORMATION:
; APPLICANT: Penner, Reinhold
; TITLE OF INVENTION: Methods of Screening for TRP4b Modulators
; FILE REFERENCE: A-71325-2/RT/NBC
; CURRENT APPLICATION NUMBER: US/10/142,649
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/351,938
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-649-2

Query Match 40.2%; Score 2448.5; DB 14; Length 1214;
Best Local Similarity 45.6%; Pred. No. 6.6e-21;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GBVNFSGGKRGKRVYVPSGVAPSLFDLIAEWHLPAPNLVSLVSGEEOPFAMKSWLR 85
Db 76 GELDTGAGRKHSNLFRLSDRTPAAVYSLVTRTWGFRAPNLVSVLGGSGPVLTWLQ 135

QY 86 DVLKGLVKAQSTGAWILTSALRYGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 136 DLRRLGLVRAAQSTGAWITGLTIGRHVGAVRDHMASTG-GTKVAVMGVAPWGV 194

QY 146 LHRRIEAAQEDFPVHY-----PEDGGSGPLCSLSDNLSHFLVPEPGKGDGLTEL 200
Db 195 RNRDTLNPKGSPFARYWRGDPED--GVQFP---LDYNSAFELVDGTHGCLGSENR 249

US-10-343-114-10
; Sequence 10, Application US/10343114
; Publication No. US20040072998A1
; GENERAL INFORMATION:
; APPLICANT: Missenbach, Ulrich
; TITLE OF INVENTION: Trp8, Trp9 and Trp10, Novel Markers for Cancer
; FILE REFERENCE: 012627-034
; CURRENT APPLICATION NUMBER: US/10/343,114
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/EP01/08309
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-114-10

Query Match 40.1%; Score 2444.5; DB 12; Length 1214;
Best Local Similarity 45.5%; Pred. No. 1.5e-216;
Matches 533; Conservative 177; Mismatches 351; Indels 111; Gaps 26;

QY 26 GBVNFSGGKRGKRVYVPSGVAPSLFDLIAEWHLPAPNLVSLVSGEEOPFAMKSWLR 85
Db 76 GELDTGAGRKHSNLFRLSDRTPAAVYSLVTRTWGFRAPNLVSVLGGSGPVLTWLQ 135

QY 86 DVLKGLVKAQSTGAWILTSALRYGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 136 DLRRLGLVRAAQSTGAWITGLTIGRHVGAVRDHMASTG-GTKVAVMGVAPWGV 194

QY 146 LHRRIEAAQEDFPVHY-----PEDGGSGPLCSLSDNLSHFLVPEPGKGDGLTEL 200
Db 195 RNRDTLNPKGSPFARYWRGDPED--GVQFP---LDYNSAFELVDGTHGCLGSENR 249

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QY 201 RLRLKHIHQAGYGGTGTGIEIPVLCVLLVNGDNPNTLIERISRAVEQAAPWLLVVGSGIA 260
D 250 RLRLSISQKTKGVGGTGTG-IDIPVLLLLIDGDEKMLTRIENATQAQPCLLVAGSGAA 308
QY 261 DVLAAVNVQPHLLVP-----KVAEQKFKFKPKSHFSDIWRVTKLLQNTSHQHL 313
D 309 DCUAEITLED--TLAPGSGGARQGEARDIRRFEPK-----GDLEVLQAQVERIMTRKELL 361
QY 314 TVVDFEQQSEEDTIVLKALVKACKSHSQEPQDYLDLKLAVADWDVDTAKSEIFNGDV 373
D 362 TVYSSE-DGSEETIVLKALVKAC--GSSEASAYLDLKLAVANVRVDAQSELFGDI 418
QY 374 EWKSCDLEEVVMDALVSNKPEFVRLFDVNGADVADELTGRLQBLVRSVSRKSLFLFLQ 433
D 419 QWRSFHLASLMDALLNDRPEFVRLSHGLSLGHFLTPMLAQLYSAAPSNSLIRNLLD 478
QY 434 RKQEEARLTLAGL--GTQQAAREPPAGPAFSLHVSRLVKDFLODAGRGYQDGRPDOR 491
D 479 QASHSAGTKAPALKGGAAELRPP-----DVGHVLRMLLGMKCAPRYPGSGAWDPH 528
QY 492 RAEGKPAKRTGQKWLIDLNOKS-----ENPWEDLFLWVLQNHHEMATYFWAMQ 542
D 529 -----PQGGFESMYLLSDKATFSLSDAGLQAPWSDLLMLNRAQMAWYFWMGS 583
QY 543 EGVAAALACKILKEMSHLETEAARATREA--KYERLALDFSECYSSEARAFALLV 600
D 584 NAVSSALGACLLLRVMALEPDAEAAARRKDLAFKFGMGVDFLGEYRSSEVRAARLL 643
QY 601 RNRCKSKTKCLHLATEADAKAFPAHDGVAFTRIWGDMAAGTPILRLGLAFPCALV 660
D 644 RCPLMGDTCQLQAWQADARAFQAQGVQSLTQKWWGDMASTTPIWALVLAFFCPPLI 703
QY 661 YTNLITF--SERAPLTGLDLOLDSLDTEKSPLYGLQSRVEELVEARAQD----- 712
D 704 YRLITFRKSEETREEL--FDMDSVINGEFGVTADPAEKTPLGVPRQSRPCCGG 761
QY 713 --RGPRAVFLTRKFKWGAQVTVFLGVNMVYPAFLFTYVLLVDFRPPQPGSPPEVT 770
D 762 RCGGRRC--LRWFHFWGVPTIFMGVNVYLLFLFLLSRVLLVDFQAP--PGSLELL 816
QY 771 LYFWMVTLVLEETROGFFDDETI-----HLVKFTLYVGNWKNKCDMVALFLFI 819
D 817 LYFMAFTLCEBELROGLSGGSLASGPGPGHASLSQRLRYLADSMNQCDLVALTCFL 876
QY 820 VGTICMLPSAFAAGRTVLAMPFWFTLRLIHFAHKGQPKIIVVERMKDVFPEFF 879
D 877 LGVGCRLTGLYHLGRTVLCIDFWFTVRLHIFTVNGKQPKIVISXMKDVFPEFF 936
QY 880 LSVLWVAYVTTQALLPHDGRLEWIFRVRVLYRPLYQIFQIPLDIDEARV---NCSTH 936
D 937 LGVWLVAYGATEGLLRPRDSDPPSILRRVYRPLYQIFQIPLQEDMDVALMEHNSCS 996
QY 937 PLLEDDSP-----SCPSLYANWLVLLVYFLVTVNLLMLLIAMFSTPQVQGNADM 991
D 997 PGFWAHPQGAQAGTCVQGANWLVLLVYFLVTVNLLMLLIAMFSTYTFKGQNSDL 1056
QY 992 FMKFORNLIVYHERPALAPFILLSHLSLTLRVFKK-----EAEKHRELERD 1042
D 1057 YWKAQRYLIRLFHSEPALAPFIVISHLRLRLQLCRPRSPQSPSPALEHFRVYLSKE 1116
QY 1043 LPDPLDKVVTWETVOKENFLSKMRKRRDSEGEVLRKTAHRVDFIAYLGLRQEKKRI 1102
D 1117 ----AERKLLTWESVHKENFILLARADKRESDESLKRTSKQVLDLALQOLGHIYEQRL 1172
QY 1103 KCLESQINCVSVLSVADVLAQG-----GGP 1129
D 1173 KVLREVOQCQSRVLGWVAEALSALLPPGP 1204
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RESULT 11

US-10-391-399-2

; Sequence 2, Application US/10391399

```
; Publication No. US20030219806A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Gilead Sciences, Inc.
; APPLICANT: Lora, Jose M.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,
; TITLE OF INVENTION: 52320, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921
; FILE REFERENCE: AND 33751 MOLECULES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/391,399
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/789,481
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 09/634,669
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 09/583,373
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/510,706
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 10/309,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/336,936
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 10/094,214
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US60/275,078
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-391-399-2

Query Match 39.6%; Score 2412.5; DB 15; Length 1129;
Best Local Similarity 45.6%; Pred. No. 1.3e-213;
Matches 528; Conservative 174; Mismatches 346; Indels 111; Gaps 26;
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QY 39 KFRVPSGVAPSVLPDLIAEWHLPAPNLVSLVGEQPFAMKSLRDVLRKGLVKAQOS 98
D 4 QFLRLSDRTDPAVYSLVTRTWGFRAPNLVSLVSGSGPVLQTLQDLRLRLVRAAQS 63
QY 99 TGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMSLGRVLRHRLIEBAQEDF 158
D 64 TGAWITVGLTIGRHVGVAVRDHMASTG-GTKVAVGAVPVGVRNDRDLINPKGSF 122
QY 159 PVHY-----PEDGSGSQPLCSLDSNLSHFLVPEPPKGDGLTELRLRLEKHISEQRA 213
D 123 FARYWRGDPED--GVQFP---LDYNSAFFLVDDTGHCLGGENRFRRLSEYSQOKT 177
QY 214 GYGGTGIEIPVLCVLLVNGDNPNTLIERISRAVEQAAPWLLVVGSGIADVLAALVNPQHL 273
D 178 GVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAQPCLLVAGSGAAQCLAEITLED--TL 234
QY 274 VP-----KVAEQKFKFKPKSHFSDIWRVTKLLQNTSHQHLTVYDFPEQSGSEL 326
D 235 AFGSGGARQGEARDIRRFEPK-----GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288
QY 327 DTIVLKALVKACKSHSQEPQDYLDLKLAVADWDVDTAKSEIFNGDVWKSCLDEEVMD 386
D 289 ETIVLKALVKAC--GSSEASAYLDLKLAVANVRVDAQSELFGDIQWRSFHLEASLMD 346
QY 387 ALVSNKPEFVRLFDVNGADVADELTGRLQBLVRSVSRKSLFLDLQKQEARLTLAGL 446
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347 ALLNDREPFVRLLSHGLSLHFTLPMRLAQYSAAPNSLIIRNLDDQASHSAGTKAPAL 406
447 --GTQARBPAGPPAPFSLHEVSRVLDKFDLQACRGFYQDGRPGDRRAEKGPAKRTGQ 504
407 KGGAAELRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH-----PGGFGES 451
505 KWLLDLNQKS-----ENPWRDLFLWALQNRHEMATYFWAMGQEGVAAALAAACKIL 555
452 MYLLSDKATSPSLDAGLQAPWSDDLWALLNPAQMAWYFWENGWNAVSSALGACLLL 511
556 KEMSHLETEAEAAARATREA--KYERLALDLFSECYNSSEARAFALLVRRNRCWSTTCLH 613
512 RVMARLEPDABEAAARRKDLAFKFGMGVDFEGCYRSSEVRAARLLRRCPLMGDATCLO 571
614 LATEADAKAPFAHGVQAFTRIWMGDMAAGTPILRLGALFCALVVTNLITP--SEEA 671
572 LAMQADARAFFAQDGVQSLITQKMGDMASTTPIWALVLAFFCPPLIYTRILITFRKSEEE 631
672 PLRTGLEDLQDLSLDTESKSPLYGLQSRVEELVEAPRAQGD-----RGPRVFLTLTR 723
632 PTREBLE--FDMDSVINGEGPVGTADPAEKTPLGVPRQSGRPGCGGRCGRRC--LRR 686
724 WRKFWGAPVTIPLGNVVMYFAPLFTVTVLLVDPRPPQGGSGGPEVTILYFWVFTLVLEEI 783
687 WFHFAGAPVTIFMGVNVSYLLFLLSRVLLVDFQAP--PGSLELLYFWAFTLLCEEL 744
784 ROGFFTDEDT-----HLVKFTLYVGDNNKCDMVAIFLPIVGTCTMLPSAFE 832
745 ROGLSGGGSLASGGPGGHASLSORLRLYLADSNQCDLVALITCFLGVGCRLLTPGLYH 804
833 AGRTVLAMDPMVFTLRLIHFALHKGOLGPKIIVVERMKDVPFFFLFSLVWLVAYGVTQ 892
805 LGRTVLCIDFWFTVRLHLHIFTVKNQKGLPKIVIVSKMKDVPFFFLFSLVWLVAYGATE 864
893 ALLHPHGRLEWIFRRVLYRPVLIQFGQIPDLDEIDARV---NCSTHPLLEDSP----- 944
865 GILLRPRDSDFFPSILRRVFRVPLQIFQGIPOQDQVLMHESNCSSEFGFWAHPGGAQ 924
945 SCPSLYANWLVLLVTTFLVTVNLLMLLIAMFSYTVQVQGNADMFWMKFORYNLIVEY 1004
925 TCVSQYANWLVLLVIFLVANILLVLLIAMFSYTVTKVQGNADLVKQAGRYLIREF 984
1005 HERPALAPPFILLSHLSLTLRVRFK-----EAEKREHLERDLPDLDQKVVTWE 1055
985 HSRPALAPPFIVISHLRLRLQLCRRPSPQSPSPALSHFRVYLSKE-----AERKLLTWE 1040
1056 TVOKENFLSKMKRRRDSGEVLRKTAHVDVFIKVLGGLRQEKRIKLESQINVCVLI 1115
1041 SVHKNFLLARADKRESDSRKRTSQKVDLALQKLGHIRBYEORLKVLEREVQOCSKV 1100
1116 VSSVADVLAQ-----GGP 1129
1101 LGWVAELSRALLPPGGP 1119

RESULT 12
US-09-789-481C-2
Sequence 2, Application US/09789481C
Patent No. US20020142377A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Curtis, Rory A.J.
APPLICANT: Lora, Jose M.
FILE REFERENCE: MNI-097CP3
CURRENT APPLICATION NUMBER: US/09/789, 481C
CURRENT FILING DATE: 2001-02-20
PRIORITY APPLICATION NUMBER: 09/510,706
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: 09/634,669
PRIORITY FILING DATE: 2000-08-08
PRIORITY APPLICATION NUMBER: 09/583,373
PRIORITY FILING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1083
TYPE: PRT
ORGANISM: Homo sapiens
US-09-789-481C-2
Query Match 38.6%; Score 2353; DB 9; Length 1083;
Best Local Similarity 45.9%; Pred. No. 3,9e-208;
Matches 515; Conservative 165; Mismatches 336; Indels 106; Gaps 25;
Qy 39 KTVRVGSGVAPSULFDLLAEWHLPAFLVSLVSGESQPPFAMKSMRLDRVLRKGLVKAQOS 98
Db 4 QFLRLSDRTDPAAYSLVTRTWGFRAPNLVVSVLGGSGPVLIQTLWQLDLRLGLVRAAQS 63
Qy 99 TGAWILTSALRVLARHVGOAVRDHSLASTSTKVRVAVGMAISLGRVILHRRILBEAQBD 158
Db 64 TGAWIVTGGHGTGRHVGVAVRDHOMASTG-GTKVAVMGVAPWGVVVRNDRTLINPKGSF 122
Qy 159 PVHY-----PEDDGGSGQPLCSLDSNLSHFTILVPPGPGKGDGUTELRLRLKHLSEORA 213
Db 123 PARYVRWGRDPED--GVQFP--LDYNTSAFFLVDDGTHGCLGGENRFRRLRESYISQOKT 177
Qy 214 GYGGTGIEIPVCLLVNGDPTLERISRAVEQAAPWLLVSGSGIADVLAAALVNOPHLL 273
Db 178 GVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAOLPCLLVAGSGGAADCLAEITLED--TL 234
Qy 274 VP-----KVAEKQKFKFPKSHFSWEDIVRWTKLLQNITSHOHLTVYDFPROGSBEL 326
Db 235 APGSGGARQGEARDIRRFPPK-----GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288
Qy 327 DTVLKALVKAACKSHSOEPQYLDLKLAVADRVDTAKSEIFNGDVEWKSCLDEVMVD 386
Db 289 ETIVLKAIVKAC--GSSEASAYLDELRLAVANVRDIAQSELFPRGDIQWRSFHLEASLMD 346
Qy 387 ALVSNKPEFVRLFVDNGADVADVLFTGLYQLYLSVSRKSLFLDLQKQBEARLTLAGL 446
Db 347 ALLNDRPBFVRLLSHGLSLHFTLPMRLAQYSAAPNSLIIRNLDDQASHSAGTKAPAL 406
Qy 447 --GTQARBPAGPPAPFSLHEVSRVLDKFDLQACRGFYQDGRPGDRRAEKGPAKRTGQ 504
Db 407 KGGAAELRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH-----PGGFGES 451
Qy 505 KWLLDLNQKS-----ENPWRDLFLWALQNRHEMATYFWAMGQEGVAAALAAACKIL 555
Db 452 MYLLSDKATSPSLDAGLQAPWSDDLWALLNPAQMAWYFWENGWNAVSSALGACLLL 511
Qy 556 KEMSHLETEAEAAARATREA--KYERLALDLFSECYNSSEARAFALLVRRNRCWSTTCLH 613
Db 512 RVMARLEPDABEAAARRKDLAFKFGMGVDFEGCYRSSEVRAARLLRRCPLMGDATCLO 571
Qy 614 LATEADAKAPFAHGVQAFTRIWMGDMAAGTPILRLGALFCALVVTNLITP--SEEA 671
Db 572 LAMQADARAFFAQDGVQSLITQKMGDMASTTPIWALVLAFFCPPLIYTRILITFRKSEEE 631
Qy 672 PLRTGLEDLQDLSLDTESKSPLYGLQSRVEELVEAPRAQGD-----RGPRVFLTLTR 723
Db 632 PTREBLE--FDMDSVINGEGPVGTADPAEKTPLGVPRQSGRPGCGGRCGRRC--LRR 686
Qy 724 WRKFWGAPVTIPLGNVVMYFAPLFTVTVLLVDPRPPQGGSGGPEVTILYFWVFTLVLEEI 783
Db 687 WFHFAGAPVTIFMGVNVSYLLFLLSRVLLVDFQAP--PGSLELLYFWAFTLLCEEL 744
Qy 784 ROGFFTDEDT-----HLVKFTLYVGDNNKCDMVAIFLPIVGTCTMLPSAFE 832
Db 745 ROGLSGGGSLASGGPGGHASLSORLRLYLADSNQCDLVALITCFLGVGCRLLTPGLYH 804
Qy 833 AGRTVLAMDPMVFTLRLIHFALHKGOLGPKIIVVERMKDVPFFFLFSLVWLVAYGVTQ 892
Db 805 LGRTVLCIDFWFTVRLHLHIFTVKNQKGLPKIVIVSKMKDVPFFFLFSLVWLVAYGATE 864
Qy 893 ALLHPHGRLEWIFRRVLYRPVLIQFGQIPDLDEIDARV---NCSTHPLLEDSP----- 944

Db	865	GLLRPRSDPFSILRRVFRPYLOIFGQIPQEDMDVALMBHSNCSSEPGFWAHPPGAQAG	924
Qy	945	SCPSIYANWLVLILLVFLIATVNLVLLMNLIIAMFSYTFQVVOGNADMFWKFORNLIVET	1004
Db	925	TCVSOYANWLVLILVFLIATVNLVLLMNLIIAMFSYTFGKVQNSDLYWKAQRYLIREF	984
Qy	1005	HERPALAPPTLLSHLSITLRRVPKK-----EAEHKREHLERDLPDLOQVVVTWE	1055
Db	985	HSRPALAPPTIVISHRLLLQLQCRPRSPQSSPALEHFRVYLSKE---AERKLLTWE	1040
Qy	1056	TVQENFLSKWEKRRRDSGEVLKTAHRVDYFIAYKLGGLRE	1097
Db	1041	SVKENFLAPARDQSDSERLKRTSQVDLALKQLGSHIRE	1082

RESULT 13

	US-10-312-354-44	
	; Sequence 44, Application US/10312354	
	; Publication No. US20040101930A1	
	; GENERAL INFORMATION:	
	; APPLICANT: INCYTE GENOMICS, INC.; JACKSON, Jennifer L.;	
	; APPLICANT: TANG, Y. Ton; YUE, Henry;	
	; APPLICANT: ELIOTT, Vicki S.; TRIBOULEY, Catherine M.;	
	; APPLICANT: LEE, Ernestine A.; RAMKUMAR, Jayalaxmi;	
	; APPLICANT: LAL, Preeti G.; XU, Yuming;	
	; APPLICANT: WARREN, Bridget A.; HAFALIA, April J. A.;	
	; APPLICANT: BAUGHN, Mariah R.; AZIMZAI, Yalda;	
	; APPLICANT: BATRA, Sajeev; BURFORD, Neil;	
	; APPLICANT: YAO, Monique G.; NGUYEN, Dannel B.;	
	; APPLICANT: LU, Dying Aina M.; CHAWLA, Narinder K.;	
	; APPLICANT: GANDHI, Ameena R.; AU-YOUNG, Janice;	
	; APPLICANT: ARVIZU, Chandra S.	
	; TITLE OF INVENTION: SECRETED PROTEINS	
	; FILE REFERENCE: PI-0133 USN	
	; CURRENT APPLICATION NUMBER: US/10/312,354	
	; CURRENT FILING DATE: 2002-12-18	
	; PRIOR APPLICATION NUMBER: US 01/19862	
	; PRIOR FILING DATE: 2001-06-20	
	; PRIOR APPLICATION NUMBER: US 60/212,890	
	; PRIOR FILING DATE: 2000-06-20	
	; PRIOR APPLICATION NUMBER: US 60/213,466	
	; PRIOR FILING DATE: 2000-06-23	
	; PRIOR APPLICATION NUMBER: US 60/214,601	
	; PRIOR FILING DATE: 2000-06-27	
	; PRIOR APPLICATION NUMBER: US 60/222,372	
	; PRIOR FILING DATE: 2000-07-31	
	; PRIOR APPLICATION NUMBER: US 60/231,435	
	; PRIOR FILING DATE: 2000-09-08	
	; PRIOR APPLICATION NUMBER: US 60/232,889	
	; PRIOR FILING DATE: 2000-09-15	
	; NUMBER OF SEQ ID NOS: 88	
	; SOFTWARE: PERL Program	
	; SEQ ID NO 44	
	; LENGTH: 1040	
	; TYPE: PRT	
	; ORGANISM: Homo sapiens	
	; FEATURE:	
	; NAME/KEY: misc feature	
	; OTHER INFORMATION: Incyte ID No: 7690129CD1	
	US-10-312-354-44	
	Query Match 35.9%; Score 2184.5; DB 16; Length 1040;	
	Best Local Similarity 45.3%; Pred. No. 1.6e-192;	
	Matches 446; Conservation 156;	

RESULT 14

RESULT 14
 US-10-369-022-48
 ; Sequence 48, Application US/10369022
 ; Publication No. US20030203947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Rosenfeld, Julie Beth

Qy	240	ISRAVEQAPWLLIVGSGGIADVLAALVNQPHLLVP-----KVAEQKFKEKFPESHFS	299
Db	114	IENATOAGLPCLLVAGSGGAADCLAETLED--TLAPGSGGARQGEARDIRRRFPK----	167
Qy	293	WEDIVRTKLLONLTSQHLLTVYDFRQEGSEELDTVILKALVACKSHSQBPQDYDEL	352
Db	168	-GDLEVIQAQVERIWRKRELLTVYSSE--DGSEEPETIVLKALVAC--GSSEASAYDEL	223
Qy	353	KLAVAMDRVDIKAEIEIFNGDVEMKSCOLEEVMVDALVSNKEFEVRLFDVNGADVADFITY	412
Db	224	RLAVAMNRVDIAQSELFRGDIQWSPHLEASLMDALLNDREFVRLLSHLSLGHFLTP	283
Qy	413	GRLOELYRSVRSKSLFDLLQKQEEEARLTLAGL--GTQQAPEPPAGPAPFASLHSEVSRL	470
Db	284	MRLAQLYSAAPSNSLIRNLLDQAQSHSAGTKAPALKGGAAELRPP-----DVGHVL	333
Qy	471	KDFLQDACRGFYQDGRPRRAEKFGAKRPTGQKWILLDLNQKS-----ENPWEDL	521
Db	334	RMLLGKWCAPRYPSGGAWDPH-----PGQFGESMYLLSDKATSPLSIDAGLGQAPMSDL	388
Qy	522	FLMAVLQNRHEMATIFYWAMGOEGVAAALAAACKILKEMSHLETEAABARATREA--KYERL	579
Db	389	LLWALLNRAQAMAYFWEMGSNAVSSALGACLLLRVVARLEPDAEEAARRKOLAFKEGM	448
Qy	580	ALDLFSECYNSERAPALLVRNRCMSKTTCLHLATEADAKAFHAGDGVQAFLTRIWWG	639
Db	449	GVDLFGCYRSSEVRAARLLLRCPLMGDMATCQLAMQADARAFFAQDGVSLLTQKWG	508
Qy	640	DMAAGTPLLGLGAFCPALVYVNLITF--SEBAPLTGLDLODLSLDEKSPLYGLQ	697
Db	509	DMASTTPIWALVAFPCPLIYTLITFRKSEBEPTEBLE--FDMOSVINGEGEVPGTAD	566
Qy	698	SRVEELVEAPRAQCD-----RGPRAVELLTRKRFWGPATVFLGNVVMFAFLFLF	749
Db	567	PAEKTPLGVPRQSGRPGCCGRCGRRC---LRWFHFWGAPVTIMGNVVSYLELLFLF	623
Qy	750	TYVLLVDFRPPQPGSPGPEVTLFYWVFTVLBEIROQFTTDEDT-----HLVKK	798
Db	624	SRVLLVDFOPAP--PGSELELLYFWAFTLLCEELRQGLSGGGGSLASGGPGPGHASLSQR	681
Qy	799	FTLYVGDNNKCDMAVLFILVIGVTCRMLPSAFAEGRTVLAMQFMWFTLRLIHFPAHKQ	858
Db	682	LRLYLADSNQCDOLVATCELLGVCGRLLPGLYHLGRVLICIDFMWFTVRLHLHFTVYKQ	741
Qy	859	LGPKIIVVERMMKDVFFFLFSLVSVLVAYGVTTQALLHPHDGRLEWFRVLRYRPLYQIF	918
Db	742	LGPKIIVVSXMKDVFFFLFGLVWLVAYGVATEGLLRPDSDFPSLLRVRVFRPLYQIF	801
Qy	919	GQIPLDEIDARV---NCSTHPLLLEBSP-----SCPSLYANMLVLLLVTLVTLVNVLL	970
Db	802	GQIPOEDMDVAMEHNSCSESPGFWAHPGQAQAGTCVSQYANMLVLLLVTLVTLVANILL	861
Qy	971	MNLLIAMFSTFOVQGNADMFKFORYNLIYVYHERPALAPDFILLSHLSLTLRRVFKK	1030
Db	862	VNLLIAMFSTYFGKVGNSDLYWQAQRYLRIRFHSRPAAPFFI WISHURLLRQLCRR	921
Qy	1031	-----EAEKHREHLERDLPDPLDQKVVTWETVQKENFIAKMEKRRDRSEGEVLKRT	1081
Db	922	PRSPQSPSALAEHFRVYLSKE---AERKLLTWESVHKENFLLARADKREDSERLKRT	977
Qy	1082	AHRVDFIAYLGLRBOEYRICKLESQINYCSVLVSSVADVTIAQG-----GGP	1129
Db	978	SKQVDIALQOLGHIREYQRLKVEREQOCCSRVLGWAEALSRSALLPPGG	1030

RESULT 14
US-10-369-022-48
; Sequence 48, Application US/10369022
; Publication NO. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth

APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
33260, 619, 15985, 69112, 2158, 224, 615, 44373,
95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
13424 MOLECULES
FILE REFERENCE: MPI02-027P1RNMNM
CURRENT APPLICATION NUMBER: US/10/369,022
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/387,536
PRIOR FILING DATE: 2002-06-10
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48
LENGTH: 1503
TYPE: PRT
ORGANISM: Homo sapiens
US-10-369-022-48

Query Match 33.5%; Score 2039; DB 12; Length 1503;
Best Local Similarity 38.8%; Pred. No. 9.6e-179;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;
26 GEVNFEGGKRGKRVFVSGVAPSVLFDLLAELHLPAPNVLVSLVSGEOPFAMKSMRLR 85
128 GDIVFTGLSQKVKYRVSDTPSSVIYHLMTHQWGLDVENLLISVTGAKNFNKKPRLK 187
86 DVLRKGLVKAAGSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKRVVAVGMASLGRV 145
188 SIFRRLGVKVAQTTGAWIITGGSTGVMKQVGEAVRDFSLSSYKEGELITITIGVATWGT 247
146 LHRRIIEEAQEDFPVHYPPDDGSGPLCSLDSNLSHFILVPEPPGKGDGLTELRLRL 205
248 HRRGLIHTGFPFAYEILDEG-QGNLTCLSNHSHFILDVDDGTHGQYGVFPLRLE 306
206 KHISEORAGYGGTGSIEIPVLCVLVNDPNTLERISRAVEQAAPWILVSGGIAVLAA 265
307 KFISEQTKERGVAIKIPVCLVWLEGGPGTLHTIDNATNGTPCVVWEGSGRVADVIAQ 365
266 LVNQP--HLVPKVAEQ--PKEPEPKHFSWEDIVRTKLLQNTISQHLITVYDFEQ 320
366 VANLPVSDITISLIQOKLSVFFQEMFET--FTESRIVETWTKIQDVRRRQLITVREGK 423
321 EGSEEDTIVLKALVKACKSHSQEPQDYLD-ELKLAVAMDRVDIAKSEIFNGVVEWKS 379
424 DGQDDVDVAILQALLKASQSDHFGHENHDLKLVANVRVDIAKSEIFMDSQWKP 483
380 LBEVMDALVSNKPEFVRLVFDNGADVADFLTYGRQLQELVRSVRSKSLFLDLQKQEEA 439
484 LHPTMTAALSNKPEFVKLFLENGVQLKEFTVWDTLLYLYENLDPSCLFHSKLQK 538
440 RLTLAIGLGTQAREPPAGP--PAFSLHVSRLVKDFLQDACRGFYQDGRGDRRR----- 492

539 -----VLVEDPBPACAPAPRLQMHVAVQLRELLGDFLTQPLYPHNDRLRLLLPV 592
493 -----AEKGPAPKPTQKWLKDLNOKSENPRDLFLWAVLQNRHENVATYFWAMQ 542
593 PHVKLVQVSLRSLYKSSGHVTF-----TMDPIRDLITWAVQNRRELAGIWAQSQ 646
543 EGVAAALAAACKILKEMSHLETEAAR---ATRAKVERLALDLFSECYSSEARAPALL 599
647 DCIAAALACSKILKELSEEDTDSSEMLALAE-EYEHRAGVFTCYRDEERAKLL 705
600 VERNRCKWTKTCLHLATEADAKAFPAHDGVQAFITRIWGDMAAGTPTLRLLGLAFLCPAL 659
706 TRVSEANGKTTCLQALAEAKMKVSHGGIOAFITKWWGQLSVNDGLWRVTLQMLAPPL 765
660 VYTNLITFSEBAPLRTGLELDLSDLSLDTESPLYGLQSRVEELVAPPAQDGRPAVF 719
766 LLTGLISFREKR-----LQD-----VGTAAA----- 786
720 LLTRWRFWAGAPVTVFVGNVYFAFLFTVYLLVDFRPPPPQSGPEVTLYFWVETLV 779
787 ---RARAPFTAPVVFVHNLISYFAFLCLFAFVLMVDFQV---PSWCECAIYLMFLSLV 840
780 LEBIROGPFDETHLVKKFTLYVGDWNKCDMAIFLFIIVGVTCTRMPLPSAFEAGRTVLA 839
841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
840 MDMVFTLRLIHFPAHKQLGPKIIVVERMMKDVFFFLFSLVWLVAVGVITQALLHPHD 899
901 LDFILFCLRLMHIFTISKTLPKIIIVRMMKDVFFFLFLLAVVWVSEGVAKQAILIHN 960
900 GRLEWIRVRLYRVLQIFGOIP--LDEIDEARVNCs---THPLLEDSPSPCS----- 948
961 RVDMLFRGAVYHSLTIFGQIPGVIGVNNFPHCSNGTDPY----KPKCPESDATQQ 1016
949 --LVANMLVILLVFLFVTLVNLMLLIAMFSYTFVQVVGADMEKFPQRYNLIVEYHE 1006
1017 RPAFPEMLTVLLCLYLFTNLLNLLIAMIENYTFQVQOEHTDQIKWFORHDLIEYHG 1076
1007 RPAAPPFILLSHLSLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFLSKM 1066
1077 RPAAPPFILLSHLQLFKRVVLTAKRHKQKLNKLENEEAALLSWEIYILKENYLNQR 1136
1067 EKRRDSEGEVLRTAHRVDPIAKYL-----GGLREQEKRIKLESQINVCVSVLSS 1118
1137 QFQQRORPEQKIEDISNKVDAMVDLLDLPKXSSM---EORLASLEEQAQTARALHW 1193
1119 VADVLAQGGPRSSQHCGEQSOLVAAD---HRGGLDGWEQPG 1157
1194 IVRTLASGFSSEADVPVLASQKAAEEDDABFGKKTKEEPG 1215

RESULT 15
US-10-405-793-21
Sequence 21, Application US/10405793
Publication No. US20030224450A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER,
TITLE OF INVENTION: LTRPG3, AND SPLICE VARIANTS THEREOF
FILE REFERENCE: D0171A CIP
CURRENT APPLICATION NUMBER: US/10/405,793
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/309,544
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 10/102,152
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 322
SOFTWARE: Patent in version 3.2
SEQ ID NO 21
LENGTH: 1503
TYPE: PRT
ORGANISM: Homo sapiens
US-10-405-793-21

Query Match 33.5%; Score 2039; DB 12; Length 1503;
Best Local Similarity 38.8%; Pred. No. 9, 6e-179;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

Qy	26	GEVNFSGSKKRGKVRVPSPGVAPSVLFDLLAEWHLPAPNLVSLVGEBOFPAMKWLR	85
Dd	:	: : : : : :	:
Dd	128	GDIVFTGLSQVKYKRVYSQDTPSSVIYHLMTQHMGLDVPNLLISVTGAKNFNNKPRLK	187
Qy	86	DVLRLKGLVKAAQSTGAWILTSALRVLGARHVGQAVRDHSLASTSTKYRVAVGNASLGTV	145
Dd	:	: : : : : :	:
Dd	188	SIFRGLVKVAQTGAIIITGGSHTGVMQWGEAVRDFSLSSYKEGELIITIGVATWGTV	247
Qy	146	LHRRILEBAQEDFPVHYPEDGGSGPLCLSDLSNLHFILVEPPGPCKGDGLTBLRLLE	205
Dd	:	: : : : : :	:
Dd	248	HRREGLIHPTGSFPAEYILDDEG-QGNLTCLDSNHSHFILVDGTHGYGVEIFLTRTELE	306
Qy	206	KHISEORAGYGTSIEIPVLICLVNGDPNTLERISRAVEOQAAPWLILVSGGGIADVLAA	265
Dd	:	: : : : : :	:
Dd	307	KFISEQTKERGGV-AIKPIVCVVLEVGGEGTLHTIDNATTGTTCVVVGGSGRVADVIAQ	365
Qy	266	LVNQP--HLLYPKVAEQ---FKEKPSKFHFSWEDIIVRTWKLLONITSHQHLITVYDFEQ	320
Dd	:	: : : : : :	:
Dd	366	VANLPVSDDITSLTOOKLSVFQEMFET--FTESRI VEWTKIQIDI VRRQLLTVFREK	423
Qy	321	EGSEBELDVIIKALKACKSHSOBPODYLD-ELKLAVAMDVRVDIAKSEIFNGDVWEKSCD	379
Dd	:	: : : : : :	:
Dd	424	DGOQDVDVAIIQALLKASRSQDHGHENWDHQKLXLAVANRVDIARSEIFMDEWQWKPSP	483
Qy	380	LEEVMVALSNKPEFFVRLFDVNGADVADFITYGRLOELYSRVSRSKSLFLDLQRKOEBA	439
Dd	:	: : : : : :	:
Dd	484	LHPTMAALTISNKPEFEVKLFLENGVOLKEFVTWDTLLLYENLDPPSCLFHSHKLQK----	538
Qy	440	RLTLAGLGTQQAAREPPAGP--PAPSLHEVSRVLKDFLQDACRGFYQDGREGDRRR-----	492
Dd	:	: : : : : :	:
Dd	539	-----VLVEDPERACAPAPRQMHHVAQVLRRELLGDFTQPPLYPRRHNDRLRLLPV	592
Qy	493	-----AEXGPAKRPTGQKWLDDLNOKNSEPNWRDLFWAVLQNRMEMATYFWAMQG	542
Dd	:	: : : : : :	:
Dd	593	PHVKLNQGVSLRSLYKRSSSHVTF-----TMDPIRDLLIWAIVQNRRELAGIIWAQSQ	646
Qy	543	EGVAAALAAACKILKEMSHLETEABAAR---ATREAKYERIALDLFSECYNSRARAFALL	599
Dd	:	: : : : : :	:
Dd	647	DCIAAALACSILKELSEEDTDSSEMLALAE-EYEHRAIGVFTCYRKDEERAQKLL	705
Qy	600	VRRNRKSKTCTCLHLATEADAKAFEAHDGVOAFLTRJWWGDMAGTPIELLGLGFLCPAL	659
Dd	:	: : : : : :	:
Dd	706	TRVSEANGKTCTCLALEAKDKMFVSHGGIOAPUTKVWNGOLSVDNGLWRTVLCMLAFP	765
Qy	660	VYTNIITFSEAPLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQGDGRGRAVF	719
Dd	:	: : : : : :	:
Dd	766	LLTGLISFREKR-----LQD-----VGTPAA-----	786
Qy	720	LLTWRFKFGAPVTVFLGNVVMYFAFLFTYVULLVDPRPPDGGSPGVTLTYFWVFTLV	779
Dd	:	: : : : : :	:
Dd	787	---RARAFFTAPVVVFHNILSYFAFLCLFAYVLMVDQPV---PSWCECAIYLWLFSLV	840
Qy	780	LEELROGFFDEETHLVKKFTLVGDNNWNKDVAIFLTVGVTCRMLPSAFEAGRIVLA	839
Dd	:	: : : : : :	:
Dd	841	CEMRQLFYDPDECGLMKKAALFSDPWNKLDVGAILLFVAGUTCRLLPATLYPGRVIIS	900
Qy	840	MDFMVFTLRLIHI FAHKQLGPKIIIVVERMMKDVFFFLLSFSLVMVAYGVTTQALLHPHD	899
Dd	:	: : : : : :	:
Dd	901	LDFILFCRLMHIFTISKTLGPKIIIIVKRWKDVFFFLFLAVWVVSFGVAKQAI IHNE	960
Qy	900	GRLEWFRVRYRPYQIFCQIP--LDEIDEARVNCS---THPLLLEDSPSCPS-----	948
Dd	:	: : : : : :	:
Dd	961	RRVDWLFPGA VHSYLTIFGIQYIDGVNFNPCHCSPNGTDPY----XPKCPESDATQQ	1016
Qy	949	--LYANWLVILLAVTELLVTNVLIMLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHE	1006
Dd	:	: : : : : :	:
Dd	1017	RPAPPFWLTVLLCLLFLFNILLNLLIAMFNFTFQQVQEHTDQIWKFORHDLIEBYHG	1076

Search completed: September 14, 2004, 00:18:05
Job time : 166 secs

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